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| Sequence 22, Application US/09384305 | Sequence 22, Application US/09384305 | Patent No. 6184028 | Patent No. 6184038 | Patent No. 61
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Patent No. 6255076
GENERAL TO PROGRATION:
APPLICANT: Widner, William
APPLICANT: Sloma, Alan
APPLICANT: Thomas, Michael D.
TITLE OF INVENTION: Methods For Producing A polypeptide In
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Best Local Similarity 100.0%; Pred. No. 5.3e-43;
Matches 185; Conservative 0; Mismatches 0;
US-10-186-042-3
US-09-769-864-58
US-09-384-305-15
US-09-258-377-19
US-08-873-479-37
US-08-972-661A-25
US-08-972-661A-25
US-09-288-377-9
US-09-031-442A-10
US-09-031-442A-10
US-09-031-442A-10
US-09-031-442A-10
US-09-091-861B-8
US-09-790-988-1
US-09-790-988-1
US-09-790-988-1
US-08-175-561A-8
US-08-175-561A-8
US-08-175-861A-8
US-08-175-861B-8
US-08-177-861B-8
US-08-177-861B-8
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US-08-177-867B-8
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/cgn2 6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2 6/ptodata/2/ina/pcTUS_COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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S-08-459-610-3
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S-08-600-908A-3
S-08-683-838A-3
S-09-182-859-3
S-09-170-670-13
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US-09-636-252A-3
US-09-545-586-13
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Maximum Match 100%
Listing first 45 summaries
                                                                        nucleic search, using sw model
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Sequence 20, Application US/09384305
Sequence 20, Application US/09384305
Patent No. 6184028
GENERAL INFORMATION:
APPLICANT: Michael D. Thomas
APPLICANT: Kimberly M. Brown
TITLE OF INVENTION: Acetylesterase Activity And Nucleic Acids Encoding Same
TITLE OF INVENTION: Acetylesterase Activity And Nucleic Acids Encoding Same
TITLE OF INVENTION: Acetylesterase Activity And Nucleic Acids Encoding Same
TITLE OF INVENTION: Acetylesterase Activity And Nucleic Acids Encoding Same
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TITLE OF INVENTION: Acetylesterase Activity And Nucleic Acids Encoding Same
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                                                                                                                           Sequence 26 Application US/09258377

Sequence 26 Application US/09258377

Patent No. 625076

GENERAL INFORMATION:
APPLICANT: Widner, William
APPLICANT: Thomas, Alan
APPLICANT: Thomas, Michael D.
ITLE OF INVENTION: Bacillus Cell
TITLE OF INVENTION: Bacillus Cell
TITLE OF INVENTION: Bacillus Cell
FILE REPERBENCE: 545.200-US
CURRENT APPLICATION WUMBER: US/09/258,377
CURRENT FILING DATE: 1999-02-26
BARLIER APPLICATION WUMBER: 09/031,442

EARLIER FILING DATE: 1998-02-26
SOFTWARE: FREESE 1998-02-26
SOFTWARE: FREESE 1998-02-26
SEQ ID NOS: 33

LENGTH: 185
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; ORGANISM: Bacillus subtilis
US-09-384-305-20
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Best Local Similarity 99.5
Matches 184; Conservative
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, ORGANISM: Bacillus
US-09-258-377-26
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US-09-384-305-20
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US-09-258-377-26
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Sequence 21, Application US/09384305

Patent No. 6184028

GENERAL INFORMATION:
APPLICANT: Michael D. Thomas
APPLICANT: Michael D. Thomas
APPLICANT: Kimberly M. Brown
TITLE OF INVENTION: Polypeptides Having Pectin
TITLE OF INVENTION: Acetylesterase Activity And Nucleic Acids Encoding Same, FILE REPERENCE: 5952.000-US
CURRENT APPLICATION NUMBER: US/09/384,305
CURRENT FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2.1
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Pred. No. 1.5e-42;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 185;
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                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 185; DB 3;
100.0%; Pred. No. 5.3e-43;
ive 0; Mismatches 0;
TITLE OF INVENTION: Bacillus Cell;
FILE REFERENCE: 5455.200-US
CURRENT APPLICATION NUMBER: US/09/258,377
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 09/031,442
BARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 27
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Best Local Similarity 99.5%;
Matches 184; Conservative
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TYPE: DNA
; ORGANISM: Bacillus subtilis
US-09-384-305-21
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Matches 185, Conservative
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US-09-258-377-27
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US-09-384-305-21
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2237 TGCAATCGATTGTTTGAGAAAGAAGAAGACGATAAAAATACCTTGTCTTGTCATCAGACA
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85.0%; Score 157.2; DB 3; Length 2604;
Best Local Similarity 98.1%; Pred. No. 5.2e-35;
Matches 159; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09264097;
Sequence 3, Application US/09264097;
Patent No. 6287826
GENERAL INFORMATION:
APPLICANT: NO. 6287826man, Barrie Edmund
APPLICANT: No. 6287826man, Barrie Edmund
APPLICANT: Hendrikesn, Hanne Vang
ITILE OF INVENTION: Enzymatic Preparation of Glucose Syrup
ITILE OF INVENTION: Enzymatic Preparation of Glucose Syrup
ITILE OF INVENTION: Enzymatic Preparation of Glucose Syrup
ITILE OF INVENTION: Enzymatic Preparation
GURRENT APPLICATION WHERE: US/08/264,097
CURRENT APPLICATION NUMBER: PA 0321/98
BARLIER FILING DATE: 1998-03-09
BARLIER FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
ELENGTH: 2604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 10216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2357 GTTATTATTTACTGATATGTAAATATAATTTGTATAAGAAATG 2402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 GACATTATTTTACTGATATGTATAATATATTTGTATAAGAAATG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

Best Local Similarity 97.0%; Pred. No. 4.2e-35;
Matches 161; Conservative 0; Mismatches 5;
COMPUTER READABLE FORM:
MEDLIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPUTER: DOS
SOFTWARE: IBM COMPUTER: DOS
SOFTWARE: IBM COMPUTER: US/08/875,154
FILING DATE: 17-JUL-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REGISTRATION NUMBER: 33,728
REGISTRATION NUMBER: 33,728
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: CHARACTERISTICS:
FENGTH: 10216 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Bacillus amyloliquefaciens
US-09-264-097-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "pMOL553"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 10216 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-264-097-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-875-154-1
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Sequence 1. Application US/08875154
Sequence 1. Se82888
GENERAL INFORMATION:
APPLICANT: JOSGENSEN, Streen Troels
ATITLE OF INVENTION: DNA Integration By Transporation
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58828860 No. 5882886disk of No. 5882888th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STRIE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ATAAAGGGGGTTGTTATTTTACTGATATGTAAAATATAATTTCTATAAGAAAATGG 180
                                                      CTGTCATCAGACAGGGTATTTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGA 120
                                                                                                                                                  ATAAAGGGGGGTTGACATTATTTTACTGATATGTATATAATATTTGTATAAGAAAATGG 180
                                                                                                                                                                                              121 ATAAAGGGGGCTTGTTATTATTTTACTGATATGTAAATTATAATTTGTATAAGAAAATGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CTGTCATCAGAGAGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAATAGGA 120
                                                                                                 61 crercarcadacadedrarrrrrrarecrercadacrercecercrerananarada 120
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     121 ATAAAGGGGGGTTGACATTATTTTACTGATATGTATAATATATTTGTATAAGAAAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CTGTCATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAATAGGA
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US-09-258-377-25

Sequence 25, Application US/09258377

Patent No. 6255076

JERREAL INFORMATION:
APPLICANT: HIGHAMYTION:
APPLICANT: Sloma, Alan
APPLICANT: Home, Miliam
APPLICANT: Home, Miliam
APPLICANT: Bloma, Alan
APPLICANT: Bloma, Alan
APPLICANT: Brownes, Michael D.
TITLE OF INVENTION: Bacillus Cell
TITLE OF INVENTION: Bacillus Cell
TITLE OF INVENTION: Bacillus Cell
CURRENT FILING DATE: 1999-02-26
CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 25

LENGTH: 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.4%; Score 180.2; DB 3 98.4%; Pred. No. 1.2e-41; ive 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 98.4
Matches 182, Conservative
                                                                                                                                                                                                                                               181 AGCTC 185
                                                                                                                                                                                                                                                                                          AGCTC 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-258-377-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-875-154-1
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i Sequence 24, Application US/08434255

i Patent No. 5621089

i GENERAL INFORMATION:

APPLICANT: Slome, Alan P.

APPLICANT: Dambmanh, Claus

APPLICANT: Dambmanh, Claus

APPLICANT: Dambmanh, Claus

APPLICANT: ARSIYON ALKALINE PROTEASE

I TILE OF INVENTION: ALKALINE PROTEASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 56210890 No. 5621089disk of No. 5621089th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10174-6-7-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              553 ATTTTTTATGCTGTCCAGACTGTCGCTGTAAAAATAGGAATAAAGGGGGGTTGTTA 712
653 ATTITITATGCTGTCCAGACTGTCCGCTGTGTAAAAATAGGAATAAAGGGGGGTTGTTA 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2604;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 TIATITIACTGATATGTATATATATTTTGTATAGAAATG 179
                                                                                                                            138 ITATITIACTGATATGTATAATATATTTGTATAAGAAATG 179
                                                                                                                                                             713 TTATTTTACTGATATGTAAATATTAATTTGTATAAGAAAATG 754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.0%; Score 157.2; DB 4 98.1%; Pred. No. 5.2e-35;
                                                                                                                                                                                                                                                                                                     APPLICANT: Andersen, Carsten
APPLICANT: Andersen, Christel T.
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Kyaerulff, Soren
TITLE OF INVENTION: Alpha-Amylase Variants
TITLE DEFENCE: 5886.200-US
CURRENT APPLICATION NUMBER: US/09/537,168
CURRENT FILING DATE: 2000-03-29
EARLIER PELING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: PA 1999 00437
EARLIER PLING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Bacillus amyloliquefaciens
US-09-537-168-5
                                                                                                                                                                                                                 RESULT 9
US-09-537-168-5
Sequence 5, Application US/09537168
Patent No. 6410295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 98.1
Matches 159; Conservative
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2604
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US-08-434-255-24
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generic 44, Application US/08459967

Factor No. 5622841

GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Dambnann, Claus
APPLICANT: Asslyng, Melle
APPLICANT: Asslyng, Dorrit
TTTLE OF INVENTION: ALKALINE PROTEASE
NUMBERS OF SEQUENCES: 27
CORRESPONDENCE ADDRESS: 27
CORRESPONDENCE ADDRESS: 27
COUNTRY: USA
STRET: New York
STRATE: BW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/459,967
FILING DATE: 02-407-107-1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 ATTITITATICCTCTCAGACTGTCCGCTGTGTAAAAAATAGGAATAAAGGGGGGTTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.2%; Score 154; DB 1; Length 162; 96.9%; Pred. No. 2.3e-34; rive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 TTATTTACTGATATGTATAATATTTGTATAAGAAATG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TTATTTTACTGATATGTAAATATATTTGTATAAGAAATG 162
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRATT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALMASIFICATION 1355
PURDSITUATION DATA:
APPLICATION NUMBER: US 08/434,255
FILING DATE: 03-MAX-1995
ATTORNEY/AGENT INFORMATION:
NAME: Agris Dr., Cheryl H.
                                                                                                                                  APPLICALLS.
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AGTIS Dr. Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764./
TELECOMMUNICATION INFORMATION:
TELEPAX: 212-867-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
IRNGTH: 162 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 96.9'
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
US-08-434-255-24
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US-08-459-871-24
  US-08-460-327-24
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                Length 162;
                                                                                                                                                                                                                                                            83.2%; Score 154; DB 1; Length 16: 96.9%; Pred. No. 2.3e-34; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TTATTTTACTGATATGTAAATATATATTTGTATAAGAAAATG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTATTTTACTGATATGTATATATATTTGTATAAGAAAATG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk
COMPUTER: IS Riopy disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,327
FILING DATE: 02-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/434,255
PRIOR APPLICATION NUMBER: US 08/434,255
ATTORNEY/AGENT INFORMATION:
NAME: AGIS DI., Cheryl H.
REFERENCE/DOCKET NUMBER: 3764.400-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764.400-US
TELECOMMONICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
REGISTRATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
TOPCLOGY: linear
US-08-459-967-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application US/08460327
Patent No. 5622850
GENERAL INFORMATION
APPLICANT: Sloma, Alan P.
APPLICANT: Dambann, Claus
APPLICANT: Dambann, Claus
APPLICANT: Dambann, Claus
APPLICANT: Asalyng, Dorrit
ITLE OF INVENTION: ALKALINE PROTEASE
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5622850418)
ADDRESSEE: No. 5622850418]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 96.9
Matches 157; Conservative
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US-08-460-327-24
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RESULT 13
US-08-459-871-24

US-08-459-871-24

j Sequence 24, Application US/08459871

j Patent No. 5550326

j GENERAL INFORMATION:

APPLICANT: Sloma, Alan P.

APPLICANT: Sloma, Helle

APPLICANT: Dambmann, Claus

APPLICANT: Asslyng, Dorrit

TITLE OF INVENTION: ALKALINE PROTEASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STREET: WAY YORK

STREET: WAY YORK
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                                                                                                                                                                                           78 ATTITITATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGAATAAAGGGGGGTTGACA 137
                                                                                                                                                                                                                                             61 ATTITITATGCTGTCCAGACTGTCCGCTGTGTAAAAATAAGGAATAAAGGGGGGGTTGTTA 120
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Length 162;
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                                                                                                18 ATCGATTGTTTGAGAAAGAAGAAGACCATAAAAATACCTTGTCTGT
                                                                                                                                                                                                                                                                                              138 TIATITIACIGATATGIATATATATITIGIATAAGAAATG 179
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COUNTRY: USA.

ZIP: 10174-6401

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRATIOS SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER:
PILING DATE: 02-UM-1995
CLASSIFICATION NUMBER: US/08/459,871
FILING DATE: 03-WAY-1995
ATTORNEY/AGBRI TNFORMATION:
APPLICATION NUMBER: US/08/434,255
ATTORNEY/AGBRI INFORMATION:
NAME: AGTIS DY., CLETY! H.
REGISTRATION NUMBER: 34,086
REFRENCE/DOCKET NUMBER: 3764.400-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
INFORMATION POR SEQ ID NO: 24:
SEQUENCE: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.2%; Score 154; DB 1; Lularity 96.9%; Pred. No. 2.3e-34; Conservative 0; Mismatches 5;
  83.2%; Score 154; DB 1; L. 96.9%; Pred. No. 2.3e-34; iive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 162 base pairs
     Query Match
Best Local Similarity 96.9
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 157; Conserv
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GENERAL INFORMATION:

APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Borchert, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TILE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58010430 No. 5801043disk of No. 5801043th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 ATTITITATIGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGAATAAAGGGGGGTTGACA 137
133 ATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAATAAGGAATAAAGGGGGGTTGTTA 192
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                                                                                                           193 riarirracidarangraaananarringraraadaaarg 234
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ZIP: 10174-6401
COUNTY: USA

ZIP: 10174-6401
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: O2-UWN-1995
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELEPHONE: 212-667-0123
TELEPHONE: 212-667-0123
                                                                                                                                                                                                                                           Sequence 3, Application US/08459610
Patent No. 5801043
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Best Local Similarity 96.9%;
Matches 157; Conservative (
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2084 base pairs
TYPE: nucleic acid
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FEATURE:
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FEATURE:
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US-08-459-610-3
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US-08-459-610-3
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STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

SIATE: New York

ZIP: 10174-6401

COUNTRY: USA

ZIP: 10174-6401

CONPUTER: BM PC compatible

COMPUTER: BM PC compatible

COMPUTER: TEM PC compatible

COMPUTER: TEM PC compatible

COMPUTER: TEM PC compatible

COMPUTER: TEM PC compatible

CONFATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/720, 899

FILING DATE: 10-OCT-1996

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/343,804

FILING DATE: 22-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: LOWING DIO: Karen A.

REGISTRATION NUMBER: 31,274

REFERENCE/DOCKET WUMBER: 4054.214-US

TELECOMPUTIONION INFORMATION:

TELECOMPUTIONIONIONE STREET AND STREET STRE
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                                                                                                                                      121 TTATTTTACTGATATGTAAAATATAATTTGTATAAGAAATG 162
                                                                                                                                                                                                                                                                   Sequence 3, Application US/08720899
Patent No. 5753460
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Soendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Mariame
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2084 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.9%;
Matches 157; Conservative
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250..342
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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LOCATION:
FEATURE:
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LOCATION:
FEATURE:
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; LOCATION:
US-08-720-899-3
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Search completed: March 19, 2004, 03:17:58 Job time: 44 secs

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Sequence:

Title: Perfect

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Result No.

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AW001963 W482d01.x
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A198938 w480012.x
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AL543011 AL543011
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BH922515 odi94C08.
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A2306757 tm0007022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Kanama, A., Bolla, B., Marra, M., Hiller, L., Kücaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Sowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Materston, R., Shin, T., Jackson, Y., Cardenas, M., Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enkarycca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
BX446359 BX446359
CC317939 TAM32-25P
AW292419 UI-H-BI2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                       BQ000230
A1998986
A1479617
B1479617
BZ072552
AU253100
AL543011
ENG101TL7
ENG22335
A1570619
EX240763
CNS01LL
EX42065
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CNS01LL
EX42067
EX42065
CNS01LL
EX42067
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CG288649
BX385059
AZ170524
BX569556
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AZ535134
AZ546631
CG184658
CG184655
BX419991
BG627035
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Glycine max
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BX356191 BX356191
AL554700 AL554700
CE808066 tigr-gss-
                                                                                                                              March 19, 2004, 01:21:15; Search time 1837 Seconds (without alignments) 3007.351 Million cell updates/sec
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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em_gas_run:;
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Maximum DB seq length: 200000000
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em_gss_pln:*
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Full-length Cardiata, Craniata, Vertebrata, Euteleostomi, Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

E 14, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length CDNA libraries and normalization
L Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12895734.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.ons.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
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ALSS4700 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI085YH07 5-PRIME, mRNA sequence.
ALSS4700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA" | for the content of the content o
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1433.r For more information about this cluster, see thtp://www.genoscope.cns.fr/
egi-bin/cluster.cgi?seq=CSODIO09BB12QP1&cluster=1433.r. Contact :
Feng Liang Bmail : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenu Genoscope sequence ID : CSODIO09BB12QP1.
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//close lib="Gm-cl048"
//cl05e lib="Gm-cl048"

     Tel: 314 286 1800
Email: set@watson.wustl.edu
Email: set@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 418.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BX356191 1000 sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI009YC24 5-PRIME, mRNA sequence.
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/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1048-2314"
/tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="l week old"
/lab_host="DH10B"
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Genoscope - Centre National de Sequencage
BP 191 91006 EYRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Pull-length cDNA libraries and normalization
Unpublished (2001)
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53.9%; Pred. No. 1.2;
:ive 0; Mismatches
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89;
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Contact: Genoscope
Genoscope - Centrer National de Sequencage
Genoscope - Centrer National de Sequencage
BP 191 91006 BVRY cedex - France
BF 191 91006 BVRY cedex - France
Email: Seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2980.r For
more information about this cluster, see
http://www.genoscope.cns.fr
cgi.bin/cluster.cgi?seq-ClobA003ZG04FPl&cluster=2980.r. Contact :
Feng Liang Email: fliang@llfetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBA003ZG04FPl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
| nol_type="mRNA" |
| nol_type="mRNA" |
| dolone="CLOBAGO135004" |
| fissue_type="PLACENTA" |
| fissue_type="PLACENTA" |
| clone="Ucctor: pCMVSPORT 6; lst strand cDNA was primed |
| note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-estrand cDNA was digested with Not I and cloned into Library was not normalized."
                                                                                                                                                                                                                            BX446359 Homo sapiens PLACENTA Homo sapiens cDNA clone CL0BA003ZG04 3-PRIME, mRNA sequence.
BX446359.1 GI:31023719
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TAM32-25P7_EC1.1 TAM32 Gallus gallus genomic clone TAM32-25P7,
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90 GICCAGACTGICCGCTGTGTAAAAATAGGAATAAAGGGGGGTTGACATTATTTTACTGA 149
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryofta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1. (Dases I to 1201)

1. W.B., Gruber, C., Jessee, J. and Polayes, D.
Full length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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                                      852
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ilarity 39.9%; Pred. No. 14;
Conservative 27; Mismatches 77;
                                                                                                                         135 GTTTATTTATTTAGACCAAGAGAAAGGAGC 168
                                                                                   150 TATGTATATATTTGTATAAGAAATGGAGC 183
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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Best Local Similarity
Matches 69; Conserv
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CC317939/c
LOCUS
DEFINITION
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BX446359/c
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VERSION
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
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/clone="CSODIO85YH07"
/tissue type="PLACENTA COT 25-NORWALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EORR V
sites of the pCWVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.

1 (bases 1 to 735)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
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                                                                                                                                                                                                                                     Gaps
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/mol type="qenomic DNA"
/strain="Standard Poodle"
/db xref="taxon:9615"
/clone lib="Dog Library"
/note="Site 1: BerXI; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003) 22875432
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                                                                                                                                                                                        21.3%; Score 39.4; DB 9; Length 1201; 39.3%; Pred. No. 8.7; ive 32; Mismatches 59; Indels 0.
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Pred. No. 14;
0; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 ATTATTTTACTGATATGTATATATATTT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         890 NTTTTTTTTTTTTTATGATACAACTT 861
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Email: ekirknes@tigr.org
Class: shotgun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (dog)
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1 Similarity 53.2%;
82; Conservative 0
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Best Local Simil
Matches 59; C
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Best Local S
Matches 82
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AW001963 461 bp mRNA linear EST 09-MAR-2000 wt82d01.x1 Soares thymus NHFTh Homo sapiens cDNA clone IMAGE:2513953 3', mRNA sequence.
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html The following repetitive elements were found in this cDNA sequence: 1-30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 AAAAATAGGAATAAAGGGGGGTTGACATTATTTTACTGATATGTATAATATATTTGTAT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.3%; Score 37.6; DB 10; Length 392; Best Local Similarity 72.1%; Pred. No. 33; Matches 49; Conservative 0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_LIB=NCI_CGAP_Lu5
TAG_SEQ=CAAC"
                                                                                                                                                 Location/Qualifiers
                                                                                           >AT_rich#Low_complexity
Seq_primer: M13 Forward
POLYA=Yee.
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AW001963
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UI-H-BIZ-agw-h-08-0-UI.sl NCI_CGAP_Sub4 Homo sapiens cDNA clone
IMAGE:2725886 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria; Aves, Neognathae; Galliformes; Phasianidae; Gallus.

1 (bases 1 to 1304)

Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Gallus gallus BAC End Reads.

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (Cases 1 to 39)
NCI (Case 1 to 10; /www.ncbi.nlm.nih.gov/ncicgap.
NCI (Case Institute, Cancer Genome Anatomy Project (CGAP);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="female"
/cell line="UCD001, inbred 256"
/clone lib="TAM32"
/note="Vector: pECBAC1; Site_1: BCOR1; Site_2: ECOR1;
/note="Vector: pECBAC1; Site_1: for library and clone ordering information: http://www.hbz.tamu.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.9%; Score 38.6; DB 28; Length 1304; 68.8%; Pred. No. 13; ive 0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                        Genome Sequencing Center
Mashington University School of Medicine
Email: submissionnewatson.wustl.edu
Insert Length: 152000 Std Error: 0.00
Seq primer: ECI TACGACTCACTATAGGGCG
Class: BAC ends
High quality sequence start: 51
High quality sequence stop: 755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Gallus gallus"
mol type="genomic DNA"
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db xref="taxon:9031"
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                                                                                                                                                                                                                                                            Contact: Richard K. Wilson
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                                        CC317939.1 GI:30711997
                                                                           Gallus gallus (chicken)
Gallus gallus
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UI-H-DIO-avp-j-04-0-UI.sl NCI_CGAP_DIO Homo sapiens cDNA clone
IMAGE:5882595 3', mRNA sequence.
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1 (bases 1 to 4462)
NCI-GAP http://www.ncbi.nlm.nih.gov/nciogap.
NCI-GAP pttp://www.ncbi.nlm.nih.gov/nciogap.
                                                                                                                                      Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
1 (base 1 to 461)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone="IMAGE:2213953"
/dev_stage="fetal"
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/clone lib="Soares thymus NHFTh"
/note="Organ: thymus, pooled; Vector: pT773D-Pac
/host="Organ: thymus, pt773D-Pac
/host="Organ: th
                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@nimage.llnl.gov) for further information. Insert Length: 696 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 448.
Location/Qualifiers
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Unpublished (1997)
Context: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
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/organism="Homo sapiens"
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AW001963.1 GI:5848879
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467 bp mRNA linear EST 08-SEP-1999 wt80e12.x1 Soares thymus NHFTh Homo sapiens cDNA clone A1989386
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I (bases I to 40. Norman to 10. Norman to 10.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -400P from Gibco
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20.3%; Score 37.6; DB 12;
Best Local Similarity 72.1%; Pred. No. 31;
Matches 49; Conservative 0; Mismatches 19;
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TAG_SEQ=ATACGCGGTC"
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Gaps .; 0

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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., M.D., M.D., Ph.D.

M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Mashington Universalty Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Conscrtium/LLNL at:

Insert Length: 885 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 446.
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/note="Corgan: lung; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_LUS was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs clone and from a boal of 5,000 clones and M. Fatima Bonaldo.
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tm32b12.xl NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2158271 3',
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Pred. No. 31;
0; Mismatches 19; Indels
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A1479617.1 GI:4372785
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Matches 49; Conservative
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Homo sapiens
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Unpublished (1997)
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Contect: Robert Strausberg, Ph.D.

Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/Anage.html
Insert Length: 701 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 465.
                                                                                                                                                          475 bp mRNA linear EST 18-DEC-1999 wels902.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2341202 3', A1697642
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1 (Dases 1 to 475)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                          1. .467
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                 High quality sequence
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Homo sapiens
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 AAGAAAT 178
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AI697642
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 70)
Ohira,M., Morohashi,A. Inuzuka,H., Shishikura,T., Kawamoto,T., Kageyama,H., Nakamura,Y., Isogai,E., Takayasu,H., Sakiyama,S., Suzuki,Y., Sugano,S., Goto,T., Sato,S. and Nakagawara,A.
Expression profiling and characterization of 4200 genes cloned from primary neuroblastomas identification of 305 genes differentially expressed between favorable and unfavorable subsets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALS43011 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE013YL22 5-PRIME, mRNA sequence.
                           700 bp mRNA linear EST 27-AUG-2003
AU253100 human favorable neuroblastoma cDNA Homo sapiens cDNA clone
Nbla01504 3', mRNA sequence.
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Catarrhini, Hominidae, Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Upublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12875489.
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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/organisme="Homo sapiens"

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/db_xref="taxon:9606"

/clone="Wbla03504"

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/clone_lib="human favorable neuroblastoma cDNA"
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Division of Biochemitery
Chiba Core Center Research Institute
Chiba Core Center Research 1817, Japan
Tel: 81-43-264-5459
Exx: 81-43-265-4459
Email: akiranak@chiba-ccri.chuo.chiba.jp.
Location/Qualifiers
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72.1%; Pred. No. 28;
iive 0; Mismatches
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EST.
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Homo sapiens
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Homo sapiens
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Matches 49; Conserv
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             RESULT 14
AU253100
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AL543011
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1kf46b09.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
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Brassica oleracea
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 699)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,
Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Umpublished (2002)
Contact: Richard K. Wilson
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                               Score 37.6; DB 9; Length 564; Pred. No. 29; 0; Mismatches 19; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448 riraraarigaariraagarraragargrarracaa 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Sequencing Center
Washington University School of Medicine
mail: submissions@watson.wustl.edu
Plate: lKf46 row: b column: 09
Seq primer: -21UPpOT forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: .... .21Urpc. .. Seq primer: -21Urpc. .. Class: shotgun
High quality sequence start: 17
High quality sequence stop: 551.
Location/Qualifiers
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BZ072552.1 GI:23690695
                                    20.3%;
                                                                                 Conservative
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170 222 us-09-834-271a-27.rst

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with a Not1-oligo(GT) primer. Five prime end enriched,
the Not I and ECRNY sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 AGAAAAGAAGAAGACCATAAAAATACCTTGTCTGTCATCAGACAGGGTATTTTTATGCT 89
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9876.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgiseq-CSODE013DF11QP1&cluster=9876.f. Contact ::
Feng Liang Email : fliang@lifetch.com URL :
http://fulllength.invitrogen.com/ TuvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODE013DF11QP1.
Location/Qualifiers
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20.2%; Score 37.4; DB 9; Length 894;

Best Local Similarity 42.3%; Pred. No. 29;

Matches 63; Conservative 22; Mismatches 64; Indels (
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Search completed: March 19, 2004, 03:16:13 Job time : 1838 secs

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Sequence 27, Appl
Sequence 6, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 7, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 5, Appli
                                                March 19, 2004, 02:14:41; Search time 745.5 Seconds (without alignments) 917.966 Million cell updates/sec
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                                                                                                    1 ggccttaagggcctgcaatc.....tgtataagaaaatggagctc
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-406-025-6
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US-10-363-332A-20
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US-09-769-864-58
US-09-769-864-58
                                                                                                                                                               Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                  nucleic search, using sw model
                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                seq length: 0
seq length: 200000000
                                                                                   US-09-834-271A-27
185
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Match Length
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                                                                                              Perfect score:
                                                                                                                     Scoring table:
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Maximum DB
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                                                                                                      Sequence:
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                                                                                    Title:
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Sequence 9, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 60, Appl Sequence 19, Appli Sequence 10, Appli Sequence 1737, Ap Sequence 1737, Ap Sequence 221, Appli Sequence 221, Appli Sequence 1736, Appli Sequence 1891, Ap Sequence 1892, Appli Sequence 1892, Appli Sequence 1897, Appli Sequence 1879, Appli Sequence 1870, Appli ô Gaps RESULT 1
US-09-834-271A-27
Sequence 27, Application US/09834271A
Sequence 27, Application US/09834271A
Sequence 27, Application US/09834271A
Publication No. US2030170876A1
GENERAL INFORMATION:
MAPLICANT: Widner, William
APPLICANT: Bloma, Alan
APPLICANT: Thomas, Michael D.
TITLE OF INVENTION: Methods For Producing A polypeptide In a
TITLE OF INVENTION: Bacillus Cell
FILE REPERENCE: 5455.200-US
CURRENT APPLICATION NUMBER: US/09/834,271A
CURRENT FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: BALLIER APPLICATION NUMBER: US/09/258,377
PRIOR FILING DATE: BALLIER APPLICATION NUMBER: BALLIER A Sequence 9, . 0 Length 185; Indels 83.2 2084 9 US-09-918-543-9
83.2 2084 12 US-09-925-5-6C-9
83.2 2084 12 US-10-664-67-58
83.2 2084 12 US-10-664-197-3
83.2 2084 14 US-10-644-197-3
83.2 2084 14 US-10-644-197-3
50.6 6837 10 US-09-928-8778-4
21.8 44 10 US-09-928-8778-4
20.3 44 10 US-09-934-271A-19
20.3 474 10 US-09-834-271A-19
20.3 67379 10 US-09-834-271A-19
20.3 67379 10 US-09-834-271A-19
20.3 67379 14 US-10-312-841-1
20.4 14924 14 US-10-311-455-198
18.9 14924 14 US-10-311-455-198
18.7 2286 12 US-10-282-122A-15549
18.7 14147 12 US-10-21-71-4A-470
18.7 2868 14 US-10-73-64-399
18.6 28588 14 US-10-73-61-399
18.6 28588 14 US-10-73-61-399
18.7 2858 14 US-10-73-61-399
18.6 28588 14 US-10-73-61-399
18.7 2858 14 US-10-73-61-399
18.8 4510 12 US-10-73-61-399
18.9 4524 14 US-10-73-61-399
18.6 28588 14 US-10-73-61-399
18.7 2858 14 US-10-73-61-399
18.8 5510 12 US-10-68-73-35-18616 Query Match
100.0%; Score 185; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.1e-41;
Matches 185; Conservative 0; Mismatches 0; ALIGNMENTS ; ORGANISM: Bacillus US-09-834-271A-27 TYPE: DNA

120

CIGICATCAGACAGGGIATITITIATATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGA

121 ATAAAGGGGGGTTGACATTTTTACTGATATGTATAATATAATTTGTATAAGAAAATGG

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Sequence 5, Application US/10406025
Publication No. US20030186380A1
GENERAL INROWATION:
APPLICANT: Thomas, Michael D.
APPLICANT: Thomas, Michael D.
APPLICANT: Thomas, Michael D.
APPLICANT: APPLICANT: Action, Alan
TITLE OF INVENTION: Activity
FILE REPRENCE: 10289.200-US
CURRENT APPLICATION NUMBER: US 60/369.192
PRIOR APPLICATION WIMBER: US 60/369.192
PRIOR APPLICATION UNMBER: US 60/369.192
PRIOR APPLICATION UNMBER: US 60/369.192
SOFTWARE: Patentin version 3.2
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                                                                             Length 185;
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                                                                                DB 10;
                                                                             Query Match 99.1%; Score 183.4; DB 10
Best Local Similarity 99.5%; Pred. No. 2.9e-41;
Matches 184; Conservative 0; Mismatches 1
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US-09-834-271A-25
Sequence 25, Application US/09834271A
; Publication No. US20030170876A1
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Best Local Similarity 99.5
Matches 184; Conservative
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AGCTC 185
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ORGANISM: Bacillus
    TYPE: DNA ORGANISM: Bacillus
                         , ORGANISM: Bac:
US-09-834-271A-26
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Sequence 6, Application US/10406025
Publication No. US20030186380A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: No. US20030186380A102ymes Biotech, Inc.
APPLICANT: Sloma, Alan
TITLE OF INVENTION: Methods for producing secreted polypeptides having L-asparaginase
TITLE OF INVENTION: activity
FILE REPERENCE: 10289.200-US
CURRENT APPLICATION NUMBER: US/10/406,025
CURRENT FILING DATE: 2003-04-01
PRIOR APPLICATION NUMBER: US 60/369,192
PRIOR FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.2
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US-09-834-271A-26
Sequence 26, Application US/09834271A
Sequence 26, Application US/09834271A
Sequence 26, Application US/09834271A
Submication No. US20030170876A1
GENERAL INFORMATION:
APPLICANT: Widner, William
APPLICANT: Thomas, Michael D.
TITLE OF INVENTION: Methods For Producing A polypeptide In a
TITLE OF INVENTION: Methods For Producing A polypeptide In a
TITLE OF INVENTION: Methods For Producing A polypeptide In a
TITLE OF INVENTION: Methods For Producing A polypeptide In a
TITLE OF INVENTION: Models: 200-104-12
FRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: EARLIER EARLIER APPLICATION NUMBER: 09/031,442
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 185
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US-10-406-025-6
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LENGTH: 185
TYPE: DNA
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US-10-406-025-6
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GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Pederacen, Poul
APPLICANT: No. US20040038375A1regaard-Madsen, Mads
APPLICANT: D080-04-US
CURRENT FILING DATE: 2003-05-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17
LENGTH: 2166
AVER OF TAXABLE 
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US-10-344-231-17

Sequence 17, Application US/10344231

Publication No. US20040038845A1

Publication No. US20040038845A1

APPLICANT: Roggen, Erwin Ludo

APPLICANT: Roggen, Erwin Ludo

TITLE OF INVENTION: Improved production of proteases with inhibitors

FILE REPERBNCE: 10064.204.US

CURRENT APPLICATION NUMBER: US/10/344,231

CURRENT FILING DATE: 2003-02-10

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.2

LENGTH: 2166
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ilarity 97.0%; Pred. No. 8.4e-34;
Conservative 0; Mismatches 5;
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ORGANISM: Artificial sequence
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Matches 161; Conserv
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Sequence 7. Application US/10466025
Publication No. US20030186380A1
Sequence 7. Application No. US20030186380A1
Sequence 7. Application No. US20030186380A1
Septicant: No. US20030186380A102ymes Biotech, Inc.
APPLICANT: Thomas, Michael D.
APPLICANT: Thomas, Michael D.
APPLICANT: Aloma, Alan
TITLE OF INVENTION: Methods for producing secreted polypeptides having L-asparaginase TILE OF INVENTION: MUMBER: US/10/406,025
CURRENT APPLICATION NUMBER: US/10/406,025
CURRENT FILING DATE: 2003-04-01
PRIOR PILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                  APPLICANT: Widner,
APPLICANT: Sloma, Alan
APPLICANT: Thomas, Michael D.
APPLICANT: Thomas, Michael D.
TITLE OF INVENTION: Methods For Producing A polypeptide In a
TITLE OF INVENTION: Bacillus Cell
FILE REFERENCE: 545.200-03
CURRENT APPLICATION NUMBER: US/09/834,271A
CURRENT APPLICATION NUMBER: US/09/258,377
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/031,442
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/031,442
PRIOR PILING DATE: BALLER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 2.3e-40;
0; Mismatches 3; Indels
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Pred. No. 2.3e-40;
0; Mismatches 3;
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Best Local Similarity 98.4%;
Matches 182; Conservative
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Best Local Similarity 98.4%;
Matches 182; Conservative
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                     GENERAL INFORMATION:
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LENGTH: 185
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LENGTH: 185
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US-10-406-025-7
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SEQ ID NO 20
US-10-363-332A-18
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Publication No. US20040038375A1
Publication No. US20040038375A1
APPLICANT: Pectersen, Poul
APPLICANT: No. US20040038375A1regaard-Madsen, Mads
APPLICANT: No. US20040038375A1regaard-Madsen, Mads
APPLICANT: No. US20040038375A1regaard-Madsen, Mads
APPLICANT: No. US20040038375A1regaard-Madsen, Mads
FILER REFERENCE: 10080.204-US
CURRENT APPLICATION NUMBER: US/10/363,332A
CURRENT FILING DATE: 2003-05-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.2
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                                                    Gaps
                    Gaps
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Sequence 18, Application US/20040038845A1

SUBJICALINEORMATION:

APPLICANT: Redgeren, From Ludo

TITLE OF INVENTION: Improved production of proteases with inhibitors
FILE REPERENCE: 10064-204-US

CURRENT APPLICANT FILING DATE: 2003-02-10

NUMBER OF SO ID NOS: 20
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                                                                                                                                                                                              134 GACATTATTTTACTGATATGTATATATATTTGTATAAGAAATG 179
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                  Indela
 Pred. No. 8.4e-34;
); Mismatches 5;
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Pred. No. 8.5e-34;
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SEQ ID NO 18
LENGTH: 2267
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Best Local Similarity 97.0%;
Matches 161; Conservative
   97.08;
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   Best Local Similarity 97.0
Matches 161; Conservative
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ORGANISM: Artificial
FEATURE:
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LENGTH: 2267
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US-10-344-231-18
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74 GGGTATTTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGAATAAAGGGGGGTT 133
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Sequence 20, Application US/10344231
Sequence 20, Application US/10344231
Sequence 20, Application US/0038845A1
Septication No. US20040038845A1
SETIMATE ROSGEN, Evalu Ludo
TITLE OF INVENTION: Improved production of proteases with inhibitors
CURRENT APPLICANT: 10064.204-US
CURRENT APPLICATION NUMBER: US/10/344,231
CURRENT FILING DATE: 2003-02-10
SOFTWARE: Patentin version 3.2
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    Length 2267;
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Score 158; DB 12;
Pred. No. 8.5e-34;
0; Mismatches 5;
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Pred. No. 9e-34;
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US-10-363-332A-20
'Sequence 20, Application US/10363332A
'Publication No. US20040038375Al
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LOCATION: (2084)..(2084);

OTHER INFORMATION: n is a, c, g,

US-10-344-231-20
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ORGANISM: Artificial sequence
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LOCATION: (2070)..(2070)
OTHER INFORMATION: n is a,
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Best Local Similarity 97.0
Matches 161; Conservative
              Query Match
Best Local Similarity 97.03
Matches 161; Conservative
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78 ATTITITATGCTGTCCAGACTGTCCGCTGTGTAAAAATAGGAAATAAAGGGGGGTTGACA 137
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Patent No. US20020068352A1
CENERAL INFORMATION:
APPLICANT: No. US20020068352A102ymes A/S
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Christel Thea
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
            DB 14; Length 2604;
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83.2%; Score 154; DB 9; Length 20
Best Local Similarity 96.9%; Pred. No. 1.1e-32;
Matches 157; Conservative 0; Mismatches 5; Indels
                                                         Indels
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                                                                                                                                                                                                                                                                                     138 TTATTTTACTGATATGTATATATATTTGTATAAGAAAATG 179
                                                                                                                                                                                                                                                                                                             Score 157.2; DB 1
Pred. No. 1.5e-33;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Djarne
APPLICANT: Nielsen, Djarne
APPLICANT: Niesen, Torben L.
APPLICANT: Kjaerulff, Soren
TITLE REPRENCE: 5368,200-US
CURRENT APPLICATION NUMBER: US/09/769,864
CURRENT APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PSESSEQ for Windows Version 3.0
SSET IN SOFTWARE: PSESSEQ for Windows Version 3.0
SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 58, Application US/09769864
Patent No. US20010039253A1
GENERAL INFORMATION:
              Query Match
Best Local Similarity 98.1%;
Matches 159; Conservative
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NAME/KEX: CDS

LOCATION: (343) ... (1794)

US-09-769-864-58
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                   APPLICANT: Pedersen Poul
APPLICANT: No. US20040038375Alregaard-Madsen, Mads
APPLICANT: No. US20040038375Alregaard-Madsen, Mads
TITLE OF INVENTION: Method For Screening Highly Active Proteases and Inhibitors
FILE REFERENCE: 10080.204-US
CURRENT APPLICANTON NUMBER: US/10/363,332A
CURRENT FILING DATE: 2003-05-27
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 20
LENGTH: 2588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 recaarcearrerreagaaaagaagaccaraaaaaraccrrecrecrecreagaca 231
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Best Local Similarity 97.0%; Pred. No. 9e-34;
Matches 161; Conservative 0; Mismatches
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GENERAL INFORMATION: US20030044954A1
GENERAL INFORMATION: US20030044954A1
GENERAL INFORMATION: Carsten
APPLICANT: Andersen, Carsten
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Kjacrulff, Soren
IIE REPERENCE: 5886.200-US
CURRENT APPLICATION UNDERE: US/10/146,327
CURRENT APPLICATION NUMBER: US/09/537,168
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR PILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR PILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR PILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FREESEQ for Windows Version 4.0
SECTION OF SEQ ID NOS: 40
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: _LOCATION: (2084) ..(2084)

: OTHER INFORMATION: n is a, c, g, or t

US-10-363-332A-20
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; ORGANISM: Bacillus amyloliquefaciens
US-10-146-327-5
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                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Construct D
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LOCATION: (2070)..(2070)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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NAME/KEY: misc feature
LOCATION: (2077)..(2077
                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial
GENERAL INFORMATION:
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Search completed: March 19, 2004, 05:16:24 Job time : 750.5 secs

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March 19, 2004, 00:21:10 ; Search time 215 Seconds (without alignments) 3655.426 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AAT85631	AAQ22579	AAN20046	AAQ88067	AAQ95032	AAX59681	AAX57596	AAA48484	ABL50568	AAS20026	AAI72215	ABL96211	AAD49392	AAV02472	AAH25109	AAD29902	AAD09917	AAZ23340	AAF62640	AAD09916	AAV38601	AAZ23330
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ALIGNMENTS

This invention describes a novel method for the production of a polypeptide in Bacillus using specific tandem or consensus promoters. The method is used to produce homologous or particularly heterologous proteins, particularly protesse, maltogues proteins, particularly series and pullularises, but also hormones, antibodies, reporters etc. The specified promoters provide increased expression of the sequence which encodes the polypeptide of the invention. After incorporation of the nucleic acid conseruct of the invention, any marker gene may be deleted, resulting in a cell that is preferred for environmental and regulatory regions. This sequence represents a Bacillus amyloliquefaciens alpha amylase amyQ promoter which is used to describe the method of the invention Tandem promoter; consensus promoter; enzyme production; hormone; amyQ; antibody; reporter; marker gene; cell regulation; alpha-amylase; ss. Production of polypeptide in Bacillus using specific promoters, particularly for producing enzymes. B. amyloliquefaciens amyQ promoter DNA #2. Claim 44; Page 90; 90pp; English. (NOVO) NOVO NORDISK BIOTECH INC. Thomas MD; ВР. 98US-00031442. 99WO-US004360. AAZ23324 standard; DNA; 185 Bacillus amyloliquefaciens. (first entry) Sloma A, WPI; 1999-561370/47. WO9943835-A2. 26-PEB-1998; 26-FEB-1999; 06-DEC-1999 02-SEP-1999 Widner W, AAZ23324;

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Query Match

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/*tag= c //rag= c //rag= c //rag= c //rag= c //race= "In column 26, a T to A mutation was said to occur at postition 116 but no such mutation was found in the sequence shown in the sequence listing of the specification"
                                                                                                                                                     The present invention relates to a method for producing a polypeptide, comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters. The Bacillus is cultivated in a medium conducive for the production of the polypeptide. Bach promoter sequence of the tandem promoter is operably linked to a nucleic acid sequence encoding the polypeptide. The tandem promoter is operably promoter comprises amyl promoter, amyl promoter, cyllink promoter or subtilisin Carlsberg gene promoter. The consensus promoters
                                                                               GCCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAAGAAGAACCATAAAAATACCTTGT
                                                                                                                                   121 ATAAAGGGGGGTTGACATTATTTTACTGATATGTATAATATTTGTATAAGAAAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus amyloliquefaciens alpha-amylase (amyQ) consensus promoter #2
                                                           CTGTCATCAGACAGGGTATTTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAATAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus cell; tandem promoter; consensus promoter; mutant; polypeptide production; amyL promoter; amyQ promoter; aprH promoter; cryIIIA promoter; subtilisin Carlsberg gene promoter; alpha-amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing a polypeptide in a Bacillus strain comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters.
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replace(135, T)
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Synthetic.
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                                                                                                                                                                         CTGTCATCAGACAGGGTATTTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAATAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated polypeptide having pectin acetylesterase activity us for degrading pectic substances and in degradation or modification acetylated pectins and plant cell walls.
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100.0%; Score 185; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.1e-42;
Matches 185; Conservative 0; Mismatches 0; Indels C
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100.0%; Score 185; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.1e-42;
Matches 185; Conservative 0; Mismatches 0; Indels (
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                         T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pectin acetylesterase; degrade; plant cell wall; ss.
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                           Sequence 185 BP; 62 A; 25 C; 42 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus amyQ promoter #2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-190946/19.
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This invention describes a novel method for the production of a polypeptide in Bacillus using specific tandem or consensus promoters. The method is used to produce homologous or particularly heterologous proteins, particularly enzymes (specifically serine protease, maltogenic alpha-amylase and pullulanase), but also hormones, antibodies, reporters etc. The specifical promoters provide increased expression of the sequence which encodes the polypeptide of the invention. After incorporation of the nucleic acid construct of the invention, any marker gene may be
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                                                                                                                                                                                                                                                         GGCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAAGAAGAAGACCATAAAAATACCTTGT 60
of the amyL promoter, amyQ promoter, aprH promoter, cryllIA promoter or subtilisin carlaberg gene promoter have the sequence TTGACA for the -35 region and TATAAT for the -10 region. The method further comprises isolating the polypeptide from the cultivation medium. The method is useful for producing a polypeptide in a Bacillus strain. The present sequence is Bacillus amyloliquefaciens alpha-amylase (amyQ) consensus mutated promoter, used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                   CTGTCATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAATAGGA
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                                                                                                                                                                                                                             GGCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAAAAGAGAGACCATAAAAATACCTTGT
                                                                                                                                                                                            Gaps
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gene; cell regulation; alpha-amylase;
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                                                                                                                                                           100.0%; Score 185; DB 4; Length 185; 100.0%; Pred. No. 3.18-42; ive 0; Mismatches 0; Indels (
                                                                                                                                Sequence 185 BP; 62 A; 25 C; 42 G; 56 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B. amyloliquefaciens amyQ promoter DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Production of polypeptide in Bacill particularly for producing enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 44; Page 90; 90pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tandem promoter; consensus antibody; reporter; marker
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                                                                                                                                                                                Best Local Similarity 100.
Matches 185; Conservative
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deleted, resulting in a cell that is preferred for environmental and regulatory regions. This sequence represents a Bacillus amyloliquefaciens alpha-amylase amyQ promoter which is used to describe the method of the
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                                                                                                                                                                                                                          61 CTGTCATCAGACAGGGTATTTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAAGGA 120
                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                       121 ATAAAGGGGGGTTGACATTATTTACTGATATGTATAATAATTTGTATAAAAAAAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to Bacillus subtilis pectin acetylesterase protein. The invention is useful for degrading a pectic substance. It is also useful for degrading soluble and insoluble pectins with varying degrees of esterification, clarification etc. The protein may be used alone or in combination with other enzymes for the degradation or modification of acetylated pectins, degradation or modification of plant
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                                                                                                                                                                                                                                                             121 ATAAAGGGGGGTTGACTATTTTACTGATATGTATAATATTTGTATAAGAAAATGG
                                                                                                                                                                               1 GGCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAAAAAGAAGAAGACCATAAAAATACCTTGT
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                                                                      Sequence 185 BP; 63 A; 25 C; 42 G; 55 T; 0 U; 0 Other;
                                                                                               Score 183.4; DB 2;
Pred. No. 8.8e-42;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pectin acetylesterase; degrade; plant cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
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                                                                                                n 99.1%;
Similarity 99.5%;
84; Conservative
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Best Local Simil
Matches 184;
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                                              invention
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Disclosure; Page 90; 90pp; English
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                                                                                                                                                                                                                                                                                                                            BP.
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                                                                                                                                                                                                                                                                                                                                                                                                              antibody; reporter; marker
                                                                                                                                                                                                                                                                                                                                                                                                    Tandem promoter; consensus
                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Matches
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                                                                                                                                                                                                                                                                             Bacillus cell; tandem promoter; consensus promoter; mutant; polypeptide production; amyL promoter; amyQ promoter; aprH promoter; crylllA promoter; alpha-amylase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for producing a polypeptide, comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters. The Bacillus is cultivated in a medium conducive for the production of the polypeptide. Each promoter sequence of the tandem promoter is operably linked to a nucleic acid sequence encoding the polypeptide. The tandem
                                                                crercateagacaggrarrrrangererecagacrererereranaaaaagga
                                                                                                    ATAAAGGGGGGTTGACATTATTTTACTGATATGTATAATATATTTTGTATAAGAAAATGG
                                                                                                                                                                                                                                                               Bacillus amyloliquefaciens alpha-amylase (amyQ) consensus promoter #1.
                                        GGCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAAAGAAGAGACCATAAAAAAACTTGT
          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing a polypeptide in a Bacillus strain comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters.
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          Indels
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 8.8e-42;
Pred. No. 8.8e
; Mismatches
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 99.5%;
                                                                                                                                                                                                        AAD09923 standard; DNA; 185
                                                                                                                                                                                                                                                                                                                     amyloliquefaciens
                                                                                                                                                                                                                                             (first entry)
          184; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-440518/47.
 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                               Synthetic
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promoter comprises amyL promoter, amyQ promoter, aprH promoter, crylIIA promoter or subtilisin Carlaberg gene promoter. The consensus promoters of the amyL promoter, amyQ promoter, amyQ promoter, oryIIIA promoter or subtilisin Carlaberg gene promoter have the sequence TTGACA for the -15 region and TATAAT for the -10 region. The method further comprises isolating the polypeptide from the cultivation medium. The method is useful for producing a polypeptide in a Bacillus strain. The present sequence is Bacillus amyloliquefaciens alpha amylase (amyQ) consensus mutated promoter, used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Production of polypeptide in Bacillus using specific promoters, particularly for producing enzymes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 185;
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 185 BP; 63 A; 25 C; 42 G; 55 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .Match 99.1%; Score 183.4; DB 4; Local Similarity 99.5%; Pred. No. 8.8e-42; es 184; Conservative 0; Mismatches 1;
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CIGICAICAGACAGGGIAITITIAIGCIGICCAGACTGICCGCIGIGIAAAAAATAGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to Bacillus subtilis pectin acetylesterase protein. The invention is useful for degrading a pectic substance. It is also useful for degrading soluble and insoluble pectins with varying degrees of esterification, clarification etc. The protein may be used alone or in combination with other enzymes for the degradation or modification of acetylated pectins, degradation or modification of plant
which encodes the polypeptide of the invention. After incorporation of the nucleic acid construct of the invention, any marker gene may be deleted, resulting in a cell that is preferred for environmental and regulatory regions. This sequence represents a Bacillus thuringiensis alpha-amylase amyQ promoter which is used to describe the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated polypeptide having pectin acetylesterase activity useful for degrading pectic substances and in degradation or modification of acetylated pectins and plant cell walls.
                                                                                                                                                                                                                                      GGCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAAGAAGAAGAACATAAAAATACCTTGT
                                                                                                                                                                                                        Gaps
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                                                                                                                                          DB 2; Length 185;
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                                                                                                              Sequence 185 BP; 62 A; 24 C; 42 G; 57 T; 0 U; 0 Other;
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                                                                                                                                          Score 180.2; DB 2;
Pred. No. 6.9e-41;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF62645 standard; DNA; 185 BP.
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                                                                                                                                                           98.48;
                                                                                                                                              97.48;
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                                                                                                                                                           Local Similarity 98.4
ses 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-190946/19.
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                                                                                   invention
                                                                                                                                                                                                                                                                                                                                                                                                  181
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                                                                                                                                              Query Match
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The present invention relates to a method for producing a polypeptide, comprises cultivating a Bacillus cell, which contains a nucleic acid comprises cultivating a tandem promoter and consensus promoters. The construct comprising a tandem promoter for the production of the pacillus is cultivated in a medium conducive for the production of the polypeptide. Each promoter sequence encoding the polypeptide. The tandem promoter comprises amyL promoter, amyQ promoter, aprH promoter, cryIIIA promoter, amyQ promoter, aprH promoter, cryIIIA promoter, amyQ promoter, aprH promoter, cryIIIA promoter, amyQ promoter, aprH promoter or subtilisin Carlsberg gene promoter, aprH promoter or subtilisin Carlsberg gene promoter the sequence TGQACA for the -35 region and TATAAT for the -10 region. The method further comprises isolating the polypeptide from the cultivation medium. The method is sequence is Bacillus amyloliquefaciens alpha-amylase (amyQ) promoter, sequence is Bacillus amyloliquefaciens alpha-amylase (amyQ) promoter, used in the exemplification of the invention. Note: This sequence is
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                                                                                                                                                                                                                                                                                                                                                   61 crercarcadacadedrarrrrranderereresadacrerecenterenaaaaradea
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                                                                                                                                      1 GGCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAAAAAAGAAGACCATAAAAATACCT
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   Length 185;
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                                                                   Indels
       4
   Score 180.2; DB 4
Pred. No. 6.9e-41;
                                                                          0; Mismatches
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Query Match
Best Local Similarity 98.4%;
Matches 182; Conservative
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Gaps

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Score 178.6; DB 2; Length 185; Pred. No. 1.9e-40; 0; Mismatches 4; Indels 0; 56 T; 0 U; 0 Other;

42 G;

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120

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61 CIGICAICAGACAGGGIATITITIAIGCIGICCAGACIGICCGCIGIGIAAAAATAGGA
                                                                                      Sequence 185 BP; 63 A; 24 C;
                                         96.5%;
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                        Query Match
Best Local Similarity 97.8
Matches 181; Conservative
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misc_feature
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                                                                                                                                                                                           CTGTCACACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGA
                                                                                                                                                    1 GGCCTTAAGGGCCCTGCAATCGATTGTTTGAGAAAGAAGAAGAAGAAGACCATAAAAATACCTTGT
                                                                                                                                                                           CTGTCATCAGGACAGGGTATTTTTTTTTGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGA
                                                                                                                             GGCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAGAAGAAGAAGACCATAAAAATACCTTGT
stated as being the same as that shown as SEQ ID NO 25 (AAD09931) in figure 21 of the specification. However the sequences differ by at position 116
                                                                                                    Gaps
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                                                                             DB 4; Length 185;
                                                                                                      Indels
                                                      Sequence 185 BP; 62 A; 24 C; 42 G; 57 T; 0 U; 0 Other;
                                                                          Ouery Match 97.4%; Score 180.2; DB 4; Best Local Similarity 98.4%; Pred. No. 6.9e-41; Matches 182; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus sp. amyQ promoter consensus DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-561370/47.
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/note="Base T is found at this location in the sequence
shown in the sequence listing of the specification
(AAD09922)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus cell; tandem promoter; consensus promoter; port promoter; polypeptide production; amyl promoter; anyl promoter; cryIIIA promoter; subtilisin Carlsberg gene promoter; alpha-amylase; ds.
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ATAAAGGGGGGTTGACATTATTTACTGATATGTATAATATAATTTGTATAAGAAAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing a polypeptide in a Bacillus strain comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus amyloliquefaciens amyQ promoter, alternative version.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 18; Fig 21; 54pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD09931 standard; DNA; 185 BP.
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us-09-834-271a-27.rng

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promoter comprises amyL promoter, amyQ promoter, aprH promoter, cryIIIA promoter or subtilisin Carlsberg gene promoter. The consensus promoters of the amyL promoter, amyQ promoter, aprH promoter, cryIIIA promoter or subtilisin Carlsberg gene promoter have the sequence TTGACA for the -35 region and TATAAT for the -10 region. The method further comprises isolating the polypeptide from the cultivation medium. The method is useful for producing a polypeptide in a Bacillus strain. The present (amyQ) promoter, used in the exemplification of the invention. Note: This sequence is stated as being the same as that shown as SEQ ID NO 25 (AADO9922) in column 43-44 of the specification. However the sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ATAAAGGGGGTTGTTATTTTTACTGATATGTAAATATAAATTTGTATAAGAAAATGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease; screening; barley; chymotrypsin inhibitor; CI-2A; laundry; detergent industry; dishwash; fabric softener; subtillsin 309; savinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-terminal Subtilisin 309-CI-2A fusion protein encoding construct A DNA.
                                                                                                                                                                                                                                                                                                             Geccritaaeeeccrecaarcearrerrigaeaaaaaaaaaeaecaraaaaracerrer
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                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                            Length 185;
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                               Sequence 185 BP; 63 A; 24 C; 42 G; 56 T; 0 U; 0 Other;
                                                                                                                                                                                                                                              DB 4;
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Pred. No. 1.9
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                                                                                                                                                                                                                                            Query Match
Best Local Similarity 97.8%;
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                differ by at position 116
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16-JUL-2002
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Chimeric.
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The invention relates to a method for screening a protease/protease continuity of a gene encoding a protease of interest. The method comprises introducing a first gene of the protease gene library and a second gene encoding a protease inhibitor into a host cell, cand a second gene encoding a protease inhibitor into a host cell, wherein the cell expresses the first and the cell associating the host cell, wherein the complex and selecting the inhibitor for complex and selecting the protease of interest and isolating the encoding gene. A complex may be used for a number of industrial applications, in particular within the detergent industry, thus, relates to a cleaning or detergent composition, comprising the complex, where hand or machine laundry detergent composition, and chine in a machine learner of encomposition or be formulated as a detergent composition for use in general household hard surface cleaning operations or be formulated for hand or machine dush washing operations. The present sequence is a construct encoding a fusion protein containing C-terminal containing of subtilisin 309 (savinase) and barley chymotrypsin inhibitor CI-capton of subtilisin 309 (savinase) and barley chymotrypsin inhibitor CI-capton of sield)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protease, allergenicity, detergent, subtilase; Sl1; Sl2; additive; protease inhibitor; barley; chymotrypsin; CI-2A; fusion protein; subtilisin; savinase; apr gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2166 BP; 610 A; 442 C; 582 G; 532 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACATTATTTTACTGATATGTATATATATTTGTATAAGAAATG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTATTATTTTACTGATATGTAAATATATATTTGTATAAGAAAATG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA construct A comprising Savinase-CI-2A fusion sequence.
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                                  Example 1; Page 47-48; 54pp; English.
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97.0%;
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24-AUG-2000; 2000US-0227501P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
                                                                                                                                                                                           The invention provides a method for producing a protease-inhibitor complex with reduced allergenicity for use in detergents. The method involves (a) constructing a fusion polynuclectide sequence in frame, the sequence comprising a first gene encoding a protease (preferably a subtilase S11 or S12) and a second gene encoding a protease inhibitor; (b) introducing the sequence into a host cell, and (c) cultivating the host cell expresses the sequence an produces a non-covalently linked complex of the protease and the inhibitor. The protease-inhibitor complex produced by the method may be used as an uncleotide sequence of a DNA construct comprising the savinase-CI-2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protease; screening; barley; chymotrypsin inhibitor; CI-2A; laundry; detergent industry; dishwash; fabric softener; subtilisin 309; savinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Subtilisin 309-CI-2A transcriptional product encoding construct B DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 GGGTATTTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGAATAAAGGGGGGGTT
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                                                                                   Producing protease-inhibitor compositions with reduced allergenicity, stability and activity for use in detergent compositions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2166 BP, 610 A, 442 C, 582 G, 532 T, 0 U, 0 Other;
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                                                                                                                                                     Example 1; Page 45-46; 52pp; English.
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05-SEP-2000; 2000US-0230017P.
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                                        WPI; 2002-242031/29.
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Bacillus lentus.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                           fusion sequence
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16-JUL-2002
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chimeric; ds.
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Pedersen PE;
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The invention relates to a method for screening a protease/protease inhibitor gene library for a gene encoding a protease of interest. The method comprises introducing a first gene of the protease gene library and a second gene encoding a protease inhibitor into a host cell, cultivating the host cell, wherein the cell expresses the first and the second genes to produce a complex of a protease and the inhibitor; dissociating the inhibitor from the complex and selecting the protease of interest and isolating the encoding gene. A complex may be used for a number of industrial applications, in particular within the detergent industry, thus, relates to a cleaning or detergent composition, preferably a laundry or dishwash composition including a laundry additive composition suitable for pre-treatment of stained fabrics and a rinse added composition, or be formulated as a detergent composition for use in general household hard surface cleaning operations or be formulated for hand or machine dish washing operations. The present sequence is a construct encoding a transcriptional fusion product containing C-terminal region of Subtilisin 309 (savinase) and barley chymotrypsin inhibitor CI-2A protein used in the invention. (Updated on 29-AUG-2003 to standardise OS field)
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Screening protease/protease inhibitor gene library for gene encoding the same, by constructing host cell having the gene, cultivating cell, dissociating complex formed between them, selecting protein and isolating
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Pred. No. 2e-34;
); Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2267 BP; 640 A; 462 C; 601 G; 564 T; 0 U; 0 Other;
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                                                                                                                                                                       Example 1; Page 48; 54pp; English
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Best Local Similarity 97.0°
Matches 161; Conservative
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Hordeum sp.
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PR 24-AUG-2000; 2000US-022750IP.

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XX
Pedersen PE;
XX
XX
Producing protease-inhibitor compositions with reduced allergenicity,
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YI
Producing protease-inhibitor compositions with reduced allergenicity,
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C complex with reduced allergenicity for use in detergents. The method
CC complex with reduced allergenicity for use in detergents. The method
CC complex with reduced allergenicity for use in detergents. The method
CC involves (a) constructing a fusion polymucleotide sequence in inframe, the
CC subtilase Sil or Si2) and a second gene encoding a protease inhibitor;
CC (b) introducing the sequence into a host cell; and (c) cultivating the
CC covalently linked complex of the protease and the inhibitor). The
CC covalently linked complex of the protease and the inhibitor). The
CC covalently linked complex of the protease and the inhibitor). The
CC covalently linked complex of the protease and the inhibitor). The
CC covalently linked complex of the protease and the inhibitor). The
CC covalently linked complex of the protease and the inhibitor). The
CC covalently sequence
CC desired as an
CC desired as such as Sequence of a DNA construct comprising the savinase-CI-2A
XX
Sequence 2267 BP; 640 A; 462 C; 601 G; 564 T; 0 U; 0 Other;
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Search completed: March 19, 2004, 01:38:17 Job time : 215 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OW nucleic - nucleic search, using sw model Run on: March 19, 2004, 00:23:20 ; Search time 1078.5 Seconds (without alignments) 7434.827 Million cell updates/sec Title: VS-09-834-271A-27 Perfect score: 185 Sequence: 1 ggccttaagggcctgcaatctgtataagaaaatggagctc 185	NUC 0, Ga eqs, 2 sfying 000000 Match	Maximum Match 100% Database: GenEmbl:* 1
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AR160503 Sequence AX088921 Sequence RD136799 Process f	AR160502 Sequence	AX088920 sequence BD136798 Process f	AR160501 Sequence AX088919 Sequence	BD136797 Process f	BD174625 Modified AR168304 Sequence	BD249244 Alpha-amy	AR215288 Sequence	BD137366 Enzymatic	140596 Sequence 24	140895 Sequence 24	IS6837 Sequence 24	V00092 Bacilius am A00155 Nucleotide	A00156 Nucleotide	A00157 Nucleotide A00158 Nucleotide	A00604 B.amyloligu	A00605 B.amyloliqu	OUIS4Z BACILIUS AM AR008285 Sequence	AR037275 Sequence	AR052145 Sequence	Akus/551 Sequence AR129916 Sequence	AR137905 Sequence	AR143262 Sequence	BDZ30131 Alpha-amy AR224261 Semience	AR285306 Sequence	AR428861 Sequence	AX244195 Sequence	AX305020 Sequence	AX370717 Sequence	AX601810 Sequence	BD077082 Alpha-amy BD085805 Alpha-amy			linear PAT 17-OCT-2001				Bacillus cell	
В ІО		AR1605	AX0889 BD1367	AR1605	BD1367	BD1746	BD2492	AR2152	BD1373									AROC	ARO3	AROE	ARIZ	AR13	AR14	BDZ3	AR26	AR42	AX24	AX3C	AX37	AX60		ALIGNMENTS		185 bp DNA	 4480			and Thomas, M.D.	A 27 03-JUL-2001; Qualifiers
% Query Match Length DE	000	999.1 185	9.1 185 9.1 185	7.4 185	7.4 185	5.0 249	5.0 2604	5.0 2604	5.0 2604	3.2 162	3.2 162	3.2 162	3.2 537	3.2 576	3.2	3.2 576	3.2 576	3.2 2084	3.2 2084	3.2 2084	3.2 2084	3.2 2084	3.2 2084	3.2 2084	3.2 2084	3.2 2084	3.2 2084	3.2 2084	3.2 2084	3.2 2084	3.2 2084 3.2 2084			37 from	60503.1 GI:16224		Unclassified. 1 (bases 1 to 185)	Sloma, Produc	S 6255076 Location/
Result No. Score	1 185 2 185 3 185	183	19 F	8 6	18	15	2 15	3 15	12	ψī	~ 00	σ,	0 -	10	w 4	25.	vοι	~ 60	0	0,	-1 C\	i m	4" (ນດ	o	σ	თი	٥,-	4 67	m	44 154 45 154		503 503	2	s SQ	SOURCE Unka	Unc.		JOURNAL PAC

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## (Dases 1 to 185)

## widner, W., Sloma, A. and Thomas, M.D.

Process for producing polypeptide in bacillus cells

Process for producing polypeptide in bacillus cells

Process for producing polypeptide in bacillus cells

NOVO NORDISK ELOTECH INC

OS Bacillus

PN 12-PEB-2002

PP 26-PEB-1999 JP 2000533574

PR 26-PEB-1999 UP 2000533574
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Widner,W., Sloma,A. and Thomas,M.D.
Methods for producing onlypeptide in a Bacillus cell
Patent: US 6255076-A 26 03-JUL-2001;
Location/Qualifiers
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Process for producing polypeptide in bacillus cells
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100.0%; Score 185; DB 6;
Best Local Similarity 100.0%; Pred. No. 9.8e-36;
Matches 185; Conservative 0; Mismatches 0;
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Location/Qualifiers
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Sequence 26 from patent US 6255076.
AR160502
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/wol_type="unassigned DNA"
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/organism="unidentified"
/mol_type="genomic DNA"
/do_xref="taxon:32644"
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Patent: WO 0114534-A 22 01-MAR-2001;
Novozymes Biotech, Inc. (US)
Location/Qualifiers
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Bacillus subtilis
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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Best Local Similarity 100.0%; Pred. No. 9.8e-36;
Matches 185; Conservative 0; Mismatches 0;
                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 9.8e-36;
Matches 185; Conservative 0; Mismatches 0;
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    .185
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     1. .185
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/wol_type="unassigned_DNA"
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linear PAT 17-OCT-2001
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JP 2002504379-A/26
12-FBB-2002
26-FBB-1999 JP 2000533574
26-FBB-1998 US 09/031442
MILLIAM WIDNER, ALAN SLOMA, MICHAEL D THOMAS
C12N15/09, C12N1/21, C12N9/54//C07K14/325, (C12N1/21, C12R1:07),
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Widner,W., Sloma,A. and Thomas,M.D.
Methods for producing a polypeptide in a Bacillus cell
Patent: US 6256076-A. 25 03-UUL-2001,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           Length 185;
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       1 (Dases 1 to 185)
Widner,W., Sloma,A. and Thomas,M.D.
Widner,W., Sloma,A. and Thomas,M.D.
Process for producing polypeptide in bacillus cells
Patent: JP 2002504379-A 26 12-PEB-2002;
NOVO NORDISK BIOTECH INC
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AR160501
AR160501.1 GI:16224474
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    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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Best Local Similarity 98.4
Matches 182; Conservative
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Best Local Similarity
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Polypeptides having pectin acetylesterase activity and nucleic acids encoding same acids encoding same
Patent: WO 0114554-A 21 01-WAR-2001;
Novozymes Biotech, Inc. (US)
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Bacillus subtilis
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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                                                                                                                                                                                                                                                                                                                linear
             Indels
 Pred. No. 2.4e-35;
                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bacillus subtilis"
/mol_type="unassigned DNA"
/db_xref="taxon:1423"
             0; Mismatches
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99.5%;
Best Local Similarity 99.5
Matches 184; Conservative
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       UP 2002504379-A/25
12-FEB-2002
26-FEB-1999 UP 2000533574
WILLIAM WIDNER, ALAN SLOMA, MICHAEL D THOMAS
C12NIS/09, C12NI/21, C12N9/54//C07K14/325, (C12N1/21, C12R1:07),
C12NIS/00
Process for producing polypeptide in bacillus cells FH Key
Location/Qualifiers
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/organism="Bacillus amyloliquefaciens"
/mol_type="genomic DNA"
/db_xref="teaxon:1390"
                                                                                                                              /organism='Bacillus'.
Location/Qualifiers
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    .185
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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BD174625
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                          61 CIGTCATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGA 120
                                                           180
                                                                                  ATABAGGGGGGTTGTTATTTTACTGATATGTABAATATTTTGTATAAGAAAATGG 180
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                                                           ATAAAGGGGGGTTGACATTATTTTACTGATATGTATAATATAATTGTATAAGAAAATGG
                                                                                                                                                                                                                                                                                                           Thomas, M.D. and Brown, K.M.
Polypeptides having pectin acetylesterase activity and nucleic acids encoding same
Patent: WO 114534-A 20 01-MAR-2001;
Novozymes Biotech, Inc. (US)
Location/Qualifiers
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Bacillus subtilis
Bacteria; Firmicutes; Bacillales; Bacillus
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JP 2002564379-A/25.
unidentified
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unclassified.
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Widner,W., Sloma,A. and Thomas,M.D.
Process for producing polypeptide in bacillus cells
Patent: JP 2003504379-A 25 12-FEB-2002;
NOVO NORDISK BIOTECH INC
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/organism="Bacillus subtilis"
/mol_type="unassigned DNA"
/db_xref="taxon:1423"
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Sequence 20 from Patent W00114534.
AX088919
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ALLAN SVENDSEN, SOEREN KJAERULFF
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28,C12P7/06,
C12P19/14,C12S11/00//(C12N9/28,C12R1:07),(C12N9/28,C12R1:10),
(C12N9/28,C12R1:125),C12N15/00,C12N5/00
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Andersen,C., Jorgensen,C.T., Bisgrd-Frantzen,H., Svendsen,A. and Kjaersen,G., Jorgensen,C.T., Bisgrd-Frantzen,H., Svendsen,A. and Alpha-amylase variants
Alpha-amylase variants
Patent: US 6410295-A 5 25-JUN-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAR-2000 JP 2000609551
30-MAR-1999 DK PA 199900437
CARSTEN ANDERSEN, CHRISTEL THEA JOERGENSEN, HENRIK BISGARD
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/organism="Bacillus amyloliquefaciens"
/mol_type="genomic DNA"
/do_xref="taxon:1390"
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Pred. No. 5.3e-29;
0; Mismatches 3;
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(2321). (2376)
(863). (2314).
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(729)...(734)
(759)...(762)
(770)...(862)
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Sequence 5 from patent US 6410295.
AR215288
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/mol_type="genomic DNA"
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ilarity 98.1%;
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Unclassified.
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Best Local Similarity
Matches 159; Conserv
Unknown.
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                         Length 249;
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Norman, B.Edmund. and Hendriksen, H. Vang.
Enzymatic preparation of glucose syrup from starch
Patent: US 6287826-A 3 11-SEP-2001;
Location/Qualifiers
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                         DB 6;
                      Match 85.0%; Score 157.2; DB 6; Local Similarity 98.1%; Pred. No. 7.4e-29; es 159; Conservative 0; Mismatches 3;
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 3 from patent US 6287826.
AR168304
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BD249244.1 GI:33059014
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Unclassified.
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Alpha-amylase variants
Patent: WO 0560059-A 5 12-0CT-2000;
NOVONORDISK AS (DK)
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YANELSLDGFRIDAAKHIKFSFLRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNK
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DITGNRSDTVKIGSDGWGFFHVNDGSVSIYVQK"
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653 ATTTTTATGCTGTCCAGACTGTCGCTGTGTAAAAAATAGGAATTAAAGGGGGGTTGTTA 712
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Bacteria, Pirmicutes, Bacillales, Bacillaceae, Bacillus.
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Best Local Similarity 98.1%; Pred. No. 5.3e-29;
Matches 159; Conservative 0; Mismatches 3; Indels
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/db_xref="taxon:1390"

/dr. .734

759 . .762

759 . .762

863 . .2314

/note="unnamed protein product"
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Sequence 5 from Patent WO0060059.
AX036892
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transl_table=
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Bacillus amyloliquefaciens

Bacillus amyloliquefaciens

Bacillus amyloliquefaciens

Bacillus amyloliquefaciens

E 1 (bases 1 to 2604)

S Norman, B.E. and Hendriksen, H.V.

Brywatic preparation of glucose syrup from starch

E Patent: JP 2002505885-A 2 26-FEB-2002;

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OS Bacillus amyloliquefaciens

PN JP 2002505885-A/2

PN JP 2002505885-A/2

PR 08-MAR-1999 DK

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BD137366 2604 bp DNA linear
Enzymatic preparation of glucose syrup from starch.
BD137366
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JP 2002505885-A/2.
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427 bp mRNA linear EST 09-DEC-2002 saugkal5.yl Gm-c1048 Glycine max cDNA clone SOYBEAN CLONE ID: CA819917
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Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylle, T., Underwood, K., Steptoe, M., Theislang, B., Allen, M., Bowers, Y., Person, B., Sauller, T., Gibbons, M., Pagesing, B., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watersten, R. and Wilson, R., Dublic Soybean BST Project Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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CA819917.1 GI:26268854
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BX446359 BX446359
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                                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Searched:

Minimum DB Maximum DB

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Scoring table:

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Caris familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Fissipedia; Canidae; Canis.

(bases 1 to 735)
Kirkness, E. Pafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                         Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8225.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=cSODIO85CD04QPl&cluster=8225.r. Contact :
Feng Liang Email : fliang@lifetech.com URL : corporation 1600
http://fulllangth.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO85CD04QPl.
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/mol type="genomic DNA"
/strain="Standard Poodle"
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39.3%; Pred. No. 6.8;
:ive 33; Mismatches
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                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI085YH07"
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The Institute for Genomic Re
Department of Enkaryctic Ger
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
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// db Aref="taxon:3847"
// clone="SOYBEAN CLONE ID: Gm-c1048-2314"
// dev stage="lu week old"
// lab_nost="bhlob"
// lab_nost=lab (GlbcoBRL). The lib_nary was constructed
// lab_nost=lab (lab_coBRL). The lib_nary at Northern
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// lab.
// lab_nost=lab.
// lab.
// lab.
// lab.
// lab.
// lab.
/
         Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is avallable through: ResGen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site:
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clone CSODI085YH07 5-PRIME, mRNA sequence.
AL554700
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High quality sequence stop: 418.
Location/Qualifiers
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Best Local Matches 9

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VERSION KEYWORDS SOURCE ORGANISM

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Exaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Exaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases I to 699)

Rash, W., Rabinovicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)

Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: subnissions@watson.wusel.edu
Plate: lkf46 row: b column: 09
Seq primer: -21UPpOT forward
Class: shotgun
High quality sequence stor: 17
High quality sequence stop: 551.
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Tetracdon nigroviridis genome survey sequence T7 end of clone
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lkf46b09.bl B.oleracea002 Brassica oleracea genomic, genomic survey
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BZO72552.1 GI:23690695
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33; Conservative
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Genoscope - Centre National de Sequencage
BP 19106 EVRY cedex - France
BP 19106 EVRY cedex - France
Genoscope - Centre National de Sequence
BP 19106 EVRY cedex - France
BP 19106 EVRY cedex - France
Email: sequescope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2980.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CLOBARO13CG4FP1&cluster=2980.r. Contact :
Feng Liang Email: fliang@alifetech.com URL :
Feng Liang Email: fliang@alifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBARO13ZG04FP1.
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BX446359 BX446359.1 GI:31023719
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/db_xref="taxon:9615"
/clone_lib="Dog_Library"
/note="Site_l: BstXI; Libraries were prepared from
peripheral_blood"
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40.5%; Pred. No. 8.4;
iive 27; Mismatches 76;
                                                                                                                                           0; Mismatches 71;
                                                                                                         21.8%; Score 40.4; DB 29;
llarity 53.9%; Pred. No. 8.9;
Conservative 0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                           150 TATGTATATATATATTTGTATAGAAATGGAGC 183
                                                                                                                                                                                                                                                                                                                                                             135 GTTTATTTATTTAGACCAAGAGAAAGGAGC 168
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Homo sapiens
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1...700
/ organism="mrassica oleracea"
/ noi_type="genomic DNA"
/ hol_type="genomic DNA"
/ db xref="taxon:3712"
/ clone_lib="B.oleracea002"
/ clone="tector: pOTW13; Whole genome shotgun library from /note="tector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
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BX356191 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens CDNA
clone CSODI009YC24 5-PRIME, mRNA sequence.
BX356191
                   Brassica oleracea
Brassica oleracea
Bukaryota deracea
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots;
rosida, eurosida II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 700)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,
Mab, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 İTİTACAAAAAAATTTTGTATAAAİTÖGAİTİTTTGGAİTTTACAAAAACAİTİTİN 372
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization (2001)
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Genoscope - Centre National de Sequencage
PP 191 91006 EVRY cedex - France
Email: seqreségenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
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                                                                                                                                                                                                                                                                                           of Medicine
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                                                                                                                                                                                                                                                                   Genome Sequencing Center
Washington University School of P
Email: submissions@watson.wustl.c
Plate: od094 row: c column: 08
Seq primer: -21UPpOT forward
Class: shotgun
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High quality sequence stop: 551
Location/Qualifiers
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
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Scrinopterygii; Neopterygii; Neopterigii; Neoteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformee;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fizames, C., Fizames, C., Elames, J., Billault, A., Quetler, F., Sautin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetracdon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                   Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Barnot, A., Fizames, C., Windker, P., Brottier, P., Quetier, F., Barrin, W. and Weissenbach, J. Bstimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence 25 (2), 235-238 (2000)
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42.9%; Pred. No. 21;
                                                                                         GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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UI-H-BIZ-agw-h-08-0-UI.S1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
UNAGE:2725886 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.inh.gov

The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonsfide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:

I.M.A.G.E. Consortium/Libra at:

www-bio.lln1.gov/bbrp/Amage.html The following repetitive elements were found in this cDNA sequence: 1-30,
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                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/mol type="mRNA"
/mol type="mRNA"
/clone="CSODIO09YC24"
/tissue type="MACRNTA"
/clone lib="Homo sapiens FLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
/note="Ist strand cDNA was primed on the NotI and Ecox V
/sites of the pCMVSPORT 6 vector. Library was normalized.
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Invitrogen. This sequence belongs to sequence cluster 1433.r For more information about this cluster, see http://www.genoscope.ns.fr/ cgi-bin/cluster.cgi?seq=CS01009BB12QP1kcluster=1433.r. Contact : Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenu Genoscope sequence ID: CS0D1009BB12QP1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 ITGITTGAGAAAAGAAGAAGACCATAAAAATACCTTGTCTGTCATCAGACAGGGTATTTT
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/db_xref="taxon:9606"
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Homo sapiens
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Emal: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/Linkl at: http://famage.lbl.gov
The following repetitive elements were found in this cDNA
sequence: 433-454, ART rich#Low_complexity (matched compliment)
Seg primer: M13 FORWARD
POLYA-Yes:
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UI-H-DIO-avp-j-04-0-UI.81 NCI_CGAP_DIO Homo sapiens cDNA clone
IMAGE:5882595 3', mRNA sequence.
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I (bases 1 to 46.)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
INSER Consortium (info@image.llnl.gov) for further information.
Insert Length: 696 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality: sequence stop: 448.
Location/Qualifiers
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Unpublished (1997)

Conteat: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmart-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LINN at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 701 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 465.
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 478. NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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20.3%; Score 37.6; DB 9; Length 475;

Query Match

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Scares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Close distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llhi.gov/bbrp/image/fmage.html

Insert Length: 685 Std Error: 0.00

Seq primmer: -40UP from Gibco

High quality sequence stop: 446.
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Matches 49; Conservative 0; Mismatches
Pred. No. 47;
0; Mismatches
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Homo sapiens (hordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 700)
RS (bhra, M., Morohash, A., Inuzuka, H., Shishikura, T., Kawamoto, T., Kaeyama, H., Nakamura, Y., Isogai, E., Takayasu, H., Saki, yama, S., Suzuki, Y., Sugano, S., Gtoo, T., Sato, S. and Nakagawara, S., Expression profiling and characterization of 4200 genes cloned from primary neuroblastomas: identification of 305 genes differentially expressed between favorable and unfavorable subsets

LE 22215148
                                 AU253100 700 bp mRNA. linear EST 27-AUG-2003 AU253100 human favorable neuroblastoma cDNA Homo sapiens cDNA clone AU253100 and AU253100 GI:34321813
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Division of Blochemistry
Chiba Cancer Center Research Institute
666-2 Nitcona, Chuoh-ku, Chiba 260-8717, Japan
Tel: 81-43-264-5459
Fax: 81-43-265-4459
Email: akiranak@chiba-ccri.chuo.chiba.jp.
Location/Qualifiers
1. 700
// Organisma.Homo sapiens"
// mol Lype="mRNA"
// db xref="texon:9606"
// clone="Nblastoma"
// tissue type="neuroblastoma"
// tissue type="neuroblastoma"
// clone_lib="human favorable neuroblastoma cDNA"
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20.3%; Score 37.6; DB 9; Length 700;
Best Local Similarity 72.1%; Pred. No. 41;
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Search completed: March 19, 2004, 03:16:12 Job time : 1842 secs

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March 19, 2004, 02:14:41; Search time 745.5 Seconds (without alignments) 917.966 Million cell updates/sec
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185
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Total number of hits satisfying chosen parameters: 2438257 segs, 1849576744 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000 Searched:

Gapop 10.0 , Gapext 1.0

IDENTITY_NUC

Scoring table:

Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCCMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_MBW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NBW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NBW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NBW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NBW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NBW_PUB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	2000		Sequence 26, Appl	Sequence 5, Appli	Sequence 27, Appl	Sequence 6, Appli	Sequence 25, Appl	Sequence 7, Appli	Sequence 17, Appl	Sequence 17, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 20, Appl	Sequence 20, Appl	Seguence 58, Appl	Sequence 9, Appli	Sequence 9, Appli
SUMMERTES	4	- !	.0 US-09-834-271A-26	.4 US-10-406-025-5	.0 US-09-834-271A-27	.4 US-10-406-025-6	.0 US-09-834-271A-25	.4 US-10-406-025-7	.2 US-10-344-231-17	.2 US-10-363-332A-17	.2 US-10-344-231-18	.2 US-10-363-332A-18	.2 US-10-344-231-20	.2 US-10-363-332A-20	US-09-769-864-58	US-09-854-346-9	US-09-918-543-9
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	, ,	SCORE	185	185	183.4	183.4	178.6	178.6	159.6	159.6	159.6	159.6	159.6	159.6	155.6	155.6	155.6
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us-0		US-10	14 US-10-184-771-3	ΩS	US-10-1	10 US-09-736-116-60	10 US-09-928-847B-49	10 US-09-834-271A-19	0 US-09-834-	10 US-09-834-271A-10		14	-SU 6	14 US-10-073-961-399	Þ	Þ	4	12 US-10-221-714A-470		9 US-09-969-347-299	σ	14 US-10-312-841-1	us-	US-09-764-891-14	16 US-10-211-179-11	SD	US-10-027-632-14	12 US-10-221-613-389	14 US-10-020-141-11
2084	2084	2084	2084	2084	2604	13222	6837	44	42	43	2141	3673778	28588	28588	179	317	3673778	14147	14147	383	9121	3673778	347	474	158001	512	827	19380	185695
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155.6	155.6	155.6	155.6	155.6	155.6	95.2	88.6	44	39	38.4	37.6	37	36	36	35.6	35.2	34.8	34.6	34.6	34.4	34.2	34.2	33.8	33.8	33.8	33.6	33.6	33.6	33.6
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APPLICANT: Widner, William
APPLICANT: Widner, William
APPLICANT: Sloma, Alan
APPLICANT: Thomas, Alan
APPLICANT: Thomas, Michael D.
TITLE OF INVENTION: Bacillus Cell
TITLE OF INVENTION: Bacillus Cell
FILE REPERENCE: 5455.200-04-12
CURRENT APPLICATION NUMBER: US/09/834,271A
CURRENT FILING DATE: 2001-04-12
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: BARLIER APPLICATION NUMBER: 09/031,442
PRIOR FILING DATE: BARLIER PILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FEASELSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 185
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100.0%; Score 185; DB 10; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.3e-41;
Matches 185; Conservative 0; Mismatches 0; Indels 0
                 ; Sequence 26, Application US/09834271A; Publication No. US20030170876A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Bacillus
-09-834-271A-26
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Sequence 6, Application US/10406025
Publication No. US20030186380A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: No. US20030186380Alozymes Biotech, Inc.
APPLICANT: Thomas, Michael D.
APPLICANT: Sloma, Alan
ITTLE OF INVENTION: Methods for producing secreted polypeptides having L-asparagina
ITTLE OF INVENTION: activity
FILE REPRENCE: 10289.200-US
CURRENT APPLICATION NUMBER: US/10/406,025
CURRENT APPLICATION NUMBER: US 60/369,192
PRIOR APPLICATION NUMBER: US 60/369,192
PRIOR FILING DATE: 2002-04-01
PRIOR FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
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Pred. No. 3.5e-41;
0; Mismatches 1; Indels
                                                                                                                        1; Indels
                                                                              Score 183.4; DB 10;
Pred. No. 3.5e-41;
                                                                                                                        0; Mismatches
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US-09-834-271A-25
Sequence 25, Application US/09834271A
Publication No. US20030170876A1
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Best Local Similarity 99.5%;
Matches 184; Conservative
                                                                                Query Match
Best Local Similarity 99.5%;
Matches 184; Conservative
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; TYPE: DNA; ORGANISM: Bacillus
US-09-834-271A-27
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US-10-406-025-6
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Publication No. US20030186380A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TO US20030186380A102ymes Biotech, Inc.
APPLICANT: No. US20030186380A102ymes Biotech, Inc.
APPLICANT: Sloma, Alan
TITLE OF INVENTION: Methods for producing secreted polypeptides having L-asparaginase
TITLE OF INVENTION: Methods for producing secreted polypeptides having L-asparaginase
TITLE OF INVENTION: METHOD SECONDS
CURRENT APPLICATION NUMBER: US/10/406,025
CURRENT FILING DATE: 2003-04-01
PRIOR FILING DATE: 2002-04-01
PRIOR FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.2
SEQ ID NO SE
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Sublication No. US2003170876A1

Sublication No. US2003170876A1

GENERAL INFORMATION:
APPLICANT: Widner, William
APPLICANT: Flomma, Alan
APPLICANT: Thomas, Michael D.
TITLE OF INVENTION: Methods For Producing A polypeptide In a
TITLE OF INVENTION: Bacillus Cell
FILE REFERENCE: 5455.200-US
CURRENT APPLICATION NUMBER: US/09/834,271A
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US/09/258,377
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 27

LENGTH: 185
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Best Local Simi
Matches 185;
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US-10-406-025-5
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APPLICANT: Pedersen, Poul APPLICANT: Pedersen, Poul APPLICANT: No. US20040038375Alregaard-Madsen, Mads TITLE OF INVENTION: Method For Screening Highly Active Proteases and Inhibitors TITLE OF INVENTION: Method For Screening Highly Active Proteases and Inhibitors CURRENT APPLICATION NUMBER 0.527

NUMBER OF SEQ ID NOS: 20

SOFTWARE PATENTY OF SEQ ID NOS: 20

SOFTWARE PATENTY OF SEQ ID NOS: 20

SOFTWARE PATENTY OF SEQ ID NOS: 20

LENGTH: 2166
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  73
                                                                                         121 ATAAAGGGGGGTTGACATTATTTACTGATATGTATAATATATTGTATAAGAAAATGG
                                               14 TGCAATCGATTGTTTGAGAAAAAGAAGACCATAAAAATACCTTGTCTTGTCATCAGACA
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Publication No. US20040038845A1
GENERAL INFORMATION:
APPLICANT: Pedersen, Poul
APPLICANT: Roggen, Erwin Ludo
TITLE OF INVENTION: Improved production of proteases with inhibitors
FILE REFERENCE: 10064.204-US
CURRENT APPLICATION NUMBER: US/10/344,231
CURRENT PILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 20
SOGTWARE: Patentin version 3.2
SEQ ID NO 17
LENGTH: 2166
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Pred. No. 3.5e-34;
0; Mismatches 4;
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Publication No. US20040038375A1
GENERAL INFORMATION:
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US-10-363-332A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial sequence
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Best Local Similarity 97.6%;
Matches 162; Conservative
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US-10-363-332A-17
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Sequence 7, Application US/10406025

Publication No. US20030186380A1

Sequence 7, Application US/10406025

Publication No. US20030186380A1

GENERAL INFORMATION:

APPLICANT: No. US20030186380Alozymes Biotech, Inc.

APPLICANT: Sloma, Michael D.

APPLICANT: Sloma, Michael D.

APPLICANT: Sloma, Alam

TITLE OF INVENTION: Activity

TITLE OF INVENTION: activity

TITLE OF INVENTION: activity

FILE PEPLICANTON NUMBER: US/10/406,025

CURRENT APPLICATION NUMBER: US 60/369,192

PRIOR FILING DATE: 2003-04-01

PRIOR FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.2
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         APPLICANT: Widner, William
APPLICANT: Widner, William
APPLICANT: Sloma, Alan
APPLICANT: Thomas, Michael D.
TITLE OF INVENTION: Methods For Producing A polypeptide In a
TITLE OF INVENTION: Bacillus Cell
TITLE OF INVENTION: Bacillus Cell
FILE REFERRNCE: 5455.200-05
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US/09/258,377
PRIOR PILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/031,442
PRIOR FILING DATE: BARLIER PILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 33
SOFTHARE: FastseQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 185
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Pred. No. 7.6e-40;
0; Mismatches 4;
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Best Local Similarity 97.8%;
Matches 181; Conservative
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GENERAL INFORMATION:
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Publication No. US20040038845A1

GENERAL INFORMATION:

APPLICANT: Redersen, Poul

APPLICANT: Roggen, Erwin Ludo

TITLE OF INVENTION: Improved production of proceases with inhibitors

TITLE OF INVENTION: Improved production of proceases with inhibitors

TITLE OF INVENTION: Improved production of proceases with inhibitors

CURRENT PELING DAIE: 2003-02-10

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.2

SEQ ID NO 20

LENGTH: 2588
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                                                                                4; Indels
                                     DB 12;
                                     Score 159.6; DB 13
Pred. No. 3.6e-34;
                                                                                0; Mismatches
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LOCATION: (2084)..(2084)
OTHER INFORMATION: n is a, c, g, or t
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US-10-363-353-32A-20
US-10-363-353-332A
Sequence 20, Application US/10363332A
Publication No. US20040038375A1
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                                     86.3%;
97.6%;
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ORGANISM: Artificial sequence
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OTHER INFORMATION: Synthetic
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LOCATION: (2070)..(2070)
OTHER INFORMATION: n is a,
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LOCATION: (2077)..(2077)
OTHER INFORMATION: n is a,
                                        Query Match
Best Local Similarity 97.6
Matches 162, Conservative
US-10-363-332A-18
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APPLICANT: Pedersen, Poul
APPLICANT: No. US20040038375Alregaard-Wadsen, Mads
APPLICANT: No. US20040038375Alregaard-Wadsen, Mads
TITLE OF INVENTION: Method For Screening Highly Active Proteases and Inhibitors
FILE REFERENCE: 10080.204-US
CURRENT APPLICATION NUMBER: US/10/363,332A
CURRENT PILING DATE: 2003-05-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.2
                                                                                                                                            232 GGGTATTTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAATAAGGAATAAAGGGGGGTT 291
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Sequence 18, Application US/10344231

Publication No. US20040038845A1

GENERAL INFORMATION:

APPLICANT: Pedersen, Poul

APPLICANT: Roggen, Erwin Ludo

TITLE OF INVENTION: Improved production of proteases with inhibitors

TITLE OF INVENTION: Improved production of proteases with inhibitors

TITLE OF INVENTION: Improved production of proteases with inhibitors

CURRENT APPLICATION NUMBER: 1064-40S

CURRENT FILING DATE: 2003-02-10

NUMBER OF SEQ ID NOS: 20

SOOFWARE: Patentin version 3.2

SEQ ID NO 18

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                      4; Indels
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Pred. No. 3.6e-34;
0; Mismatches 4.
  Pred. No. 3.5e-34;
                      0; Mismatches
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Publication No. US20040038375A1
GENERAL INFORMATION:
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Best Local Similarity 97.6%;
Matches 162; Conservative
  97.68;
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Best Local Similarity 97.6
Matches 162; Conservative
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LENGTH: 2267
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TYPE: DNA ORGANISM: Bacillus amyloliquefaciens
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LOCATION: (343)..(1794)

COTHER INFORMATION: BAN

US-09-854-346-9
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US-09-918-543-9
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                              APPLICANT: Pedersen, Poul Participant Mads (1870-1875) Mads (1870-1875) Mads (1870-1875) Mads (1870-1875) Mads (1870-1875) Mathie OF INVENTION: Method For Screening Highly Active Proteases and Inhibitors FILE REFERENCE: 10080.204-US (1870-1875) MACHING MUMBER: US/10/363,332A (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NOS: 20 (1870-1876) MUMBER OF SEQ ID NO
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NAME/KEY: misc feature

COCATION: (2077)..(2077)

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FEATURE:

NAME/KEY: misc feature

COCATION: (2084)..(2084)

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ORGANISM: Bacillus amyloliquefaciens
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LOCATION: (2070)..(2070)
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; LOCATION: (343)...(1794)
US-09-769-864-58
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ORGANISM: Artificial
GENERAL INFORMATION:
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                                                                                                                                                                    78 ATTITITATGCIGICCAGACTGTCCGCTGTGTAAAAAAAAGGAATAAAGGGGGGTTGACA 137
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| Sequence 9, Application US/09854346
| Sequence 9, Application US/09854346
| Patent No. US20020068352Alozymes A/S
| APPLICANT: No. US20020068352Alozymes A/S
| APPLICANT: Nielsen, Allan
| APPLICANT: Nielsen, Bjarne Ronfeldt
| APPLICANT: Nielsen, Bjarne Ronfeldt
| TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
| FILE REFERENCE: 6140.200-US
| CURRENT APPLICATION NUMBER: US/09/854,346
| CURRENT FILING DATE: 201.05-11
| NUMBER OF SEQ ID NOS: 15
| SEQ ID NO 9
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Petent No. US2002015574A1

GENERAL INFORMATION:
GENERAL THIPORMATION:
APPLICANT: No. US20020155574A10zymes A/S

APPLICANT: Kjaerulff, Soren
APPLICANT: Kjaerulff, Soren
APPLICANT: Fuglsang, Claus Crone
APPLICANT: Fuglsang, Claus Crone
FILE REPERSACE: 10062.200-US
FILE REPERSACE: 10062.200-US
CURRENT APPLICATION NUMBER: US/09/918,543
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84.1%; Score 155.6; DB 9; Length 2084;
Best Local Similarity 97.5%; Pred. No. 4.5e-33;
Matches 158; Conservative 0; Mismatches 4; Indels 0;
   DB 9; Length 2084;
Query Match

84.1%; Score 155.6; DB 9; Length:
Best Local Similarity 97.5%; Pred. No. 4.5e-33;
Matches 158; Conservative 0; Mismatches 4; Indels
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
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1511
155.
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ALIGNMENTS

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US-09-184-305-21

US-09-184-305-21

Sequence 21, Application US/09384305

Sequence 21, Application US/09384305

Sequence 21, Application US/09384305

GENERAL INFORMATION:

APPLICANT: Kimberly M. Brown

TITLE OF INVENTION: Polypeptides Having Pectin

TITLE OF INVENTION: Polypeptides Having Pectin

TITLE OF INVENTION: Acetylesterase Activity And Nucleic Acids Encoding Same

FILE REPERENCE: 5952.000-US

CURRENT APPLICATION NUCLE: 1999-08-26

CURRENT APPLICATION NUCLE: 1999-08-26

NUMBER OF SEQ ID NOS: 25

SEQ ID NOS: 25

SEQ ID NO 21

LENGTH: 185
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100.0%; Score 185; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 9.7e-43;
Matches 185; Conservative 0; Mismatches 0; Indels
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Batcht No. 6255076

BAPLICANT: Widner, William

APPLICANT: Sloma, Alana

APPLICANT: Thomas, Michael D.

TITLE OF INVENTION: Methods For Producing A polypeptide In a
                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Bacillus subtilis
US-09-384-305-21
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US-09-258-377-26
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Sequence 20, Application US/09384305
Patent No. 6184028
GENERAL INFORMATION
APPLICANT: Michael D. Thomas
APPLICANT: Kimberly M. Brown
TITLE OF INVENTION: Polypeptides Having Pectin
TITLE OF INVENTION: Acetyleaterase Activity And Nucleic Acids Encoding Same
FILE REFERENCE: 5952.000-US
CURRENT APPLICATION NUMBER: US/09/384,305
CURRENT FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 185;
                                                                                                         US-09-28-3/7-2)

DS-09-28-3/7-2)

Patent No. 6255076

GENERAL INPORMATION:

APPLICANT: Widner, William

APPLICANT: Sloma, Alan

APPLICANT: Sloma, Alan

TITLE OF INVENTION: Methods For Producing A polypeptide In a TITLE OF INVENTION: Methods For Producing A polypeptide In a TITLE OF INVENTION: Methods For Producing A polypeptide In a TITLE OF INVENTION: Methods For Producing A polypeptide In a TITLE OF INVENTION: Methods For Producing A polypeptide In a TITLE OF INVENTION NUMBER: US/09/258,377

CURRENT FILING DATE: 1999-02-26

EARLIER APPLICATION NUMBER: 09/031,442

FRAILER FILING DATE: 1998-02-26

NUMBER OF SEQ ID NOS: 33

SOFFWARE: FREISEQ FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.1%; Score 183.4; DB 3; 99.5%; Pred. No. 2.7e-42; iive 0; Mismatches 1;
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US-09-384-305-20
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Best Local Similarity 99.5
Matches 184; Conservative
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     181 AGCTC 185
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, ORGANISM: Bacillus
US-09-258-377-27
                                                                        RESULT 4
US-09-258-377-27
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US-09-384-305-20
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Sequence 22, Application US/09384305
Patent No. 6184028
GENERAL INFORMATION:
CENERAL INFORMATION:
APPLICANT: Michael D. Thomas
APPLICANT: Kimberly M. Brown
TITLE OF INVENTION: Polypeptides Having Pectin
TITLE OF INVENTION: Acctylesterase Activity And Nucleic Acids Encoding Same FILE REFERENCE: 5952.000-US
CURRENT APPLICATION NUMBER: US/09/384,305
CURRENT FILING DATE: 1999-08-26
NUMBER OF SEC ID NOS: 25
SOFTWARE: FREUSER FOR Windows Version 3.0
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100.0%; Pred. No. 9.7e-43;
iive 0; Mismatches 0;
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TILLE OF INVENTION: Bacillus Cell
FILE REFERENCE: 5455.200-02
CURRENT APPLICATION NUMBER: US/09/258,377
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 09/031,442
EARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-09-384-305-22
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Best Local Similarity 99.5'
Matches 184; Conservative
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Best Local Similarity 100.
Matches 185; Conservative
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) ORGANISM: Bacillus
US-09-258-377-26
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US-09-384-305-22
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LENGTH: 185
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405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTCATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAAAGGA
GGCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAAAAAGAAGAGCCATAAAAATACCTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 185;
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Widner, William

APPLICANT: Thomas, Michael D.

TITLE OF INVENTION: Bachlods For Producing A polypeptide In a TITLE OF INVENTION: Bachlods Cell

FILE REFERENCE: 5455.200-US

CURRENT APPLICATION NUMBER: 08/09/258,377

CURRENT PILICATION NUMBER: 09/031,442

EARLIER FILING DATE: 1999-02-26

SARLIER PILING DATE: 1998-02-26

NUMBER OF SEQ ID NOS: 33

SOTTWARE: FastSEQ for Windows Version 3.0
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                                                                                                            121 ATAAAGGGGGTTGACATTATTTTACTGATATGTATAATATATT
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Patent No. 588288
Patent No. 588288
Patent No. 588288
Patent No. 588288
APPLICANT: Jorgensen, Streen Troels
TITLE OF INVENTION: DNA Integration By Transporation NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58828880 No. 5882888disk of No. 5882
ATREET: 405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 178.6; DB 3;
Pred. No. 5.8e-41;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/09258377
Patent No. 6255076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.5%;
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Best Local Similarity 97.8
Matches 181; Conservative
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CORGANISM: Bacillus
US-09-258-377-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUDRESSEE: No. 56210890 No. 5621089disk of No. 5621089th America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 159.6; DB 2; Length 10216; Pred. No. 2.5e-35; 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2357 GTTATTATTTACTGATATGTAAATATATTATTGTATAAGAAATG 2402
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APPLICATION NUMBER: US/08/434,255
                                         COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTHWARE: FESTEEC for Windows Version 2.0
SUBJECTION DATA:
APPLICATION NUMBER: US/08/875,154
FILING DATE: 17-JUL-1997
CLASSIFFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lambling, Blias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 33,728
TELECOMONICATION INFORMATION:
TELECHONE: 212-867-0123
TELECHANS: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application US/08434255; Patent No. 5621089; Patent LINFORMATION: Alan P. APPLICANT: Outrrup, Helle; APPLICANT: Dambmain, Claus APPLICANT: Dambmain, Claus APPLICANT: ABSING, DOrrit; TITLE OF INVENTION: ALKALINE PROTEASE; CORRESPONDENCE ADDRESS: ADDRESSEE: No. 56210899 No. 5621089418)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "pMOL553"
                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10216 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ATTORNEY/AGENT INFORMATION:
NAME: Agris Dr., Cheryl H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 97.6%;
Matches 162; Conservative
COMPUTER READABLE FORM MEDIUM TYPE: Disket:
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SSEE: No. 56228500 No. 5622850disk of No. 5622850th America, Inc.
T: 405 Lexington Avenue, 64th Floor
New York
                                                                                                                                                                                                                                              61 ATTITITATGCTGTCCAGACTGTCCGCTGTGTAAAATAAGGAATAAAGGGGGGGTTGTTA 120
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                                        Length 162;
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                                                                              4; Indels
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                                                                                                                                                                                                                                                                                                                               TTATTTTACTGATATGTAAATATATTTGTATAAGAAATG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPY disk

COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPY disk

COMPUTER: IMP PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,327

FILING DATE: 02-UUN-1995

CLASSIFICATION: 435

PRICH APPLICATION NUMBER: US 08/434,255

FILING DATE: 03-MAX-1995

ATTORNEY/AGENT INFORMATION:

NAME: AGTIS DY., CHeryl H.

REGISTRATION UNMBER: 34,086

REGISTRATION NUMBER: 3764
                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 155.6; DB 1
Pred. No. 1.4e-34;
0; Mismatches 4
                                      Score 155.6; DB 1
Pred. No. 1.4e-34;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dandwann, Claus
APPLICANT: Dandwann, Claus
APPLICANT: Aaalyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56228500 No. 5622850die
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 3764.400-US TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/08460327
Patent No. 5622850
GENERAL INFORMATION:
                                      84.1%;
97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 97.5%;
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 base pairs nucleic acid
                                        Query Match
Best Local Similarity 97.5
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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CITY: New
STATE: Ne
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US-08-460-327-24
US-08-459-967-24
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Patent No. 5622841

GENERAL INFORMATION:
APPLICANT: Outtrup, Helle
APPLICANT: Outtrup, Helle
APPLICANT: Dambann, Claus
APPLICANT: Dambann, Claus
APPLICANT: Asslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56228410 No. 5622841th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                              09
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COUNTRY: USA
ZIP: 10.74-6401
ZIP: 10.74-6401
ZIP: 10.74-6401
COMPUTER READABLE FORM:
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,967
FILING DATE: 02-UN-1995
CLASSIFICATION NUMBER: US 08/434,255
FILING DATE: DT., GREYJ H.
APPLICATION NUMBER: 34,086
ATTORNEY/AGENT INFORMATION:
NAME: AGTIS DT., GREYJ H.
REGISTRATION NUMBER: 3764.400-US
TELECOMUNICATION NUMBER: 3764.400-US
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                       Score 155.6;
Pred. No. 1.46
                                                                                                                                                                                                                                                                                                                  0; Mismatches
                  REFERENCE/DOCKET NUMBER: 3764.400-US
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHRACTERISTICS:
LENGTH: 162 base pairs
TYPE: nucleic acid
STRANDENESS: single
  34,086
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.5%;
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
ENGER: 162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
REGISTRATION NUMBER:
                                                                                                                                                                                                                 linear
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CITY: New York
STATE: New York
                                                                                                                                                                                                            ;
US-08-434-255-24
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NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
US-08-720-899-3
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ADDRESSER:
CORRESPONDENCE ADDRESS:

STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIF: 10174-6401

COMPUTER: EDAPP disk
COMPUTER: EDAPP disk
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: O3-MA-1995
CLASSIFICATION NUMBER: US 08/434,255
FILING DATE: 03-MA-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 3764.400-US
FILING DATE: 03-MA-1995
ATTORNEY/AGENT NUMBER: 374.066
REFERENCE/DOCKET NUMBER: 374.066
REFERENCE/DOCKET NUMBER: 374.066
REFERENCE/DOCKET NUMBER: 374.066
REFERENCE/DOCKET NUMBER: 374.066
REFERENCE/DOCKET NUMBER: 374.066
REFERENCE/DOCKET NUMBER: 3764.400-US
TELEPHONE: 212-867-0123
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 base pairs
TTPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTITITITATGCTGTCCAGACTGTCCGCTGTGTAAAAATAAGGAATAAAGGGGGGTTGTTA 120
61 ATTTTTTATGCTGTCCAGACTGTCCGCTGTGAAAAATAAGGAATAAAGGGGGGTTGTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                        138 TTATTTTACTGATATGTATAATATATTTGTATAAGAAATG 179
                                                                              121 TTATTTTACTGATATGTAAATATAATTTGTATAAGAAAATG 162
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                                                                                                                                                                                                                                                   APPLICANT: Sloma, Alan P.
APPLICANT: Outring, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Aaslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
CORRESPONDENCE ADDRESS:
                                                                                                                                                             US-08-459-871-24
Sequence 24, Application US/08459871
Patent No. 5850326
GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-08-720-899-3
; Sequence 3, Application US/08720899
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97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 97.5
Matches 158; Conservative
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78 ATTITITATGCTGTCCAGACTGTCCGCTGTGTAAAAAAGGAATAAAGGGGGGGTTGACA 137
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CITY: Now York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 Arcgairgirigagaaaagaagaccaraaaaaraccrogrogrogrogacagacag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTATTTTACTGATATATATATATTTGTATAAGAAATG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tratritacrdarateraaararaarrirgraraagaaarg 234
                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

ZIP: 10174-6401

COMPUTER READBLE FORM:
MEDIUM TYPE: Flogpy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,899
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 155.6; DB 1;
Pred. No. 2.3e-34;
0; Mismatches 4;
Patent No. 5753460
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-459-610-3; Sequence 3, Application US/08459610; Patent No. 5801043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: LOWNEY Dr., Karen A.
REGIGSTRATION NUMBER: 31,274
REFRENCE/DOCKET NUMBER: 4054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 97.5%;
Matches 158; Conservative
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250..342
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343..1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT: BOLLER, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Marianne
APPLICANT: Thalleresen, Marianne
APPLICANT: Thalleresen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLES VARIANTS
MUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5830837c No. 5830837th America, Inc.
STREET: New York
STATE: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 ATTITITATGCTGTCCAGACTGTCCGCTGTGTAAAAAAAAAGGAATAAAGGGGGGTTGACA 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 TIATITIACIGATAIGIATAATATAATITIGIATAAGAAATG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 TTATTTTACTGATATGTAAATATAATTTGTATAAGAAATG 234
                                                                                                                                                                                                                                                                   COMPREY: USA

CONTRY: USA

CIP: 1014-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATE: 22-NOV-1994

FILING DATE: 22-NOV-1994

CLASSIPICATION: 435

ATTORNEY/AGBWT INFORMATION:
NAME: LOWING NUMBER: 4054.214-US

REGISTRATION NUMBER: 31,274

REGISTRATION NUMBER: 31,274

REFERENCE/DOCKET NUMBER: 4054.214-US

TELEPHONE: 212-87-0123

TELEPHONE: 212-87-0555

INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 2084 base pairs

STRANDBDNESS: single

STRANDBDNESS: single
    Bisgaard-Frantzen, Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08687399; Patent No. 5928381
GENERAL INFORMATION:
APPLICANT: Toft, Annette H.
APPLICANT: Marcher, Dorthe
APPLICANT: Pedereen, Homes H.
APPLICANT: Nilsson, Thomas E.
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Best Local Similarity 97.5%;
Matches 158; Conservative (
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; LOCATION:
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US-08-687-399-3
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Best Local Similarity 97.5%; Pred. No. 2.3e-34;
Matches 158; Conservative 0; Mismatches 4; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610 FILING DATE: 02-3UN-1995 CLASSIFICATION: 435 PRIOR APPLICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804 FILING DATE: 22-NOV-1994 ATTORNEY/AGENT INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
ITILE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSE: No. 58010430 No. 5801043disk of NSTREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10174-6401
COMPUTER READBLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 3. Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: LOWING DE., KAREN A.
REGISTRATION NUMBER: 31,274
REFRENCE/DOCKET NUMBER: 4054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2084 base pairs TYPE: nucleic acid STRANDEDNESS: single
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343..1791
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LOCATION: 250..1794
FEATURE:
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CITY: New York
STATE: New York
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LOCATION:
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TITLE OF INVENTION: A Combined Desizing and Bleaching
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
COTY: New York
CONFUTER: 10174-6401
COMPUTER: New York
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CONFUTER: New York
CONFUTER: Desired States of America
MEDIUM TYPE: Floppy disk
COMPUTER: New York
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MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
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March 19, 2004, 00:21:10; Search time 215 Seconds (without alignments) 3655.426 Million cell updates/sec
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1 ggccttaagggcctgcaatc.....tgtataagaaaatggagctc 185
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GenCore version 5.1,6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                              3373863 seqs, 2124099041 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N Geneseq 29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                           Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqn2003bs:* geneseqn2003cs:* geneseqn2004s:* 10:

geneseqn2001bs:* geneseqn2003as:*

geneseqn2001as: geneseqn2002s:*

geneseqn2000s:*

	Description	Aaz23323 B. amylol	Aaf62646 Consensus	Aad09923 Bacillus	Aaz23324 B. amylol	Aaf62647 Consensus	Aad09924 Bacillus	ın	Aad09931 Bacillus	N	'n	C)	Aad34433 C-termina		Aad34434 Subtilisi	Abl40499 DNA const	Aad34436 PamyL ATG	Ab140501 DNA const	Aat39279 Transposo	Aat85631 BAN promo	Aaa93677 Bacillus	Aca61514 Modified	Aaa93678 Modified	Aaq22579 Sequence
SUMMARIES	ŒΙ	AAZ23323	AAF62646	AAD09923	AA223324	AAF62647	AAD09924	AAZ23325	AAD09931	AAZ23322	AAF62645	AAD09922	AAD34433	ABL40498	AAD34434	ABL40499	AAD34436	ABL40501	AAT39279	AAT85631	AAA93677	ACA61514	AAA93678	AAQ22579
	DB	23	4	4	N	4	4	7	4	7	4	4	9	9	9	9	9	ø	7	7	m	7	m	7
	% Query Match Length DB	185	185	185	185	185	185	185	185	185	185	185	16	2166	26	26	58	TT)	10216	162	4	4	~	537
	% Query Match	6	100.0	100.0	1.66	99.1	99.1	97.4	97.4	96.5	96.5	96.5	86.3	86.3	86.3	86.3	86.3	86.3	4.	84.1	84.1	84.1	84.1	84.1
	Score	185	185	185	183.4	183.4	183.4	180.2	180.2	178.6	78	178.6		59	159.6	159.6	159.6	159.6		155.6	'n	'n	155.6	155.6
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Aan20046 Bacillus	Aaq88067 Bacillus	_	Aax59681 DNA encod	Aax57596 Wild type					-	Aaz21079 Bacillus	•	Aad49392 pMOL995 p		Aah25109 Nucleotid	Aad29902 Plasmid p	Aad09917 Oligo #2	Aaz23340 Bacillus	Aaf62640 amyQ prom	Aad09916 Oligo #1	Aav38601 PCR prime	Aaz23330 Bacillus
AAN20046	AAQ88067	AAQ95032	AAX59681	AAX57596	AAA48484	ABL50568	AAS20026	AAI72215	ABL96211	AAZ21079	AAA37850	AAD49392	AAV02472	AAH25109	AAD29902	AAD09917	AAZ23340	AAF62640	AAD09916	AAV38601	AAZ23330
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576	2084	2084	2084	2084	2084	2084	2084	2084	2084	2604	2604	6661	2083	13222	6837	48	44	44	44	42	42
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84	84	84	84	84	84	84	8	84	84	84	84	84	77	51	4	25	23	23.8	23	2	21
155.6	155.6	155.6	155.6	155.6	155.6	155.6	155.6	155.6	155.6	155.6	155.6	155.6	143.6	95.2	88.6	48	44	44	44	e O	en en
24	25	56	27	28	53	30	31	32	33	34	n D	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

Tandem promoter; consensus promoter; enzyme production; hormone; amyQ; antibody; reporter; marker gene; cell regulation; alpha-amylase; ss. B. amyloliquefaciens amyQ promoter DNA #1. AAZ23323 standard; DNA; 185 BP Bacillus amyloliquefaciens. 06-DEC-1999. (first entry) WO9943835-A2. AAZ23323;

99WO-US004360. 26-FEB-1999; 02-SEP-1999.

(NOVO) NOVO NORDISK BIOTECH INC.

98US-00031442.

26-FEB-1998;

Thomas MD; Widner W, Sloma A,

WPI; 1999-561370/47.

Production of polypeptide in Bacillus using specific promoters, particularly for producing enzymes.

Claim 44; Page 90; 90pp; English.

This invention describes a novel method for the production of a polypeptide in Bacillus using specific tandem or consensus promoters. The method is used to produce homologous or particularly heterologous proteins, particularly enzymes (specifically serine procease, maltogenic alpha-amylase and pullulanase), but also hormones, antibodies, reporters etc. The specified promoters provide increased expression of the sequence which encodes the polypeptide of the invention. After incorporation of the nucleic acid construct of the invention, any marker gene may be deleted, resulting in a cell that is preferred for environmental and regulatory regions. This sequence represents a Bacillus amyloliquefaciens alpha-amylase amyQ promoter which is used to describe the method of the

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Bacillus cell; tandem promoter; consensus promoter; mutant; polypeptide production; amyL promoter; amyQ promoter; aprH promoter; cryIIIA promoter; subtilisin Carlsberg gene promoter; alpha-amylase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method for producing a polypeptide, comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters. The Bacillus is cultivated in a medium conducive for the production of the polypeptide. Bach promoter sequence of the tandem promoter is operably linked to a nucleic acid sequence encoding the polypeptide. The tandem promoter comprises amy promoter, any promoter, april promoter, cryllib promoter or subtilisin Carlaberg gene promoter. The consensus promoter of the amy promoter, any promoter, april promoter, any promoter, april promoter or subtilisin Carlaberg gene promoter. The consensus promoter of subtilisin Carlaberg gene promoter, april promoter or subtilisin Carlaberg gene promoter.
                                         CTGTCATCAGACAGGGTATTTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAAAGGA
              Producing a polypeptide in a Bacillus strain comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters.
                                                                                                                                                                                                                                                                                                                                  Bacillus amyloliquefaciens alpha-amylase (amyQ) consensus promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated polypeptide having pectin acetylesterase activity useful for degrading pectic substances and in degradation or modification of acetylated pectins and plant cell walls.
                                                                                                                                                     121 ATAAAGGGGGGTTGACATTATTTTACTGATATGTATAATTTTGTATAAAATGG
                                                                                                 GGCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAGAAGAAGAACATAAAAATACCTTGT
                                                                                                                 CIGICATCAGACAGGGIATITITIATGCTGTCCAGACTGTCCGCTGTGTAAAAAAAAGGA
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                                            Length 185;
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                A; 25 C; 42 G; 55 T; 0 U; 0 Other;
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                                         100.0%; Score 185; DB 2;
100.0%; Pred. No. 1.6e-41;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                               AAF62646 standard; DNA; 185 BP.
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Best Local Similarity 100.
Matches 185, Conservative
                                                                      185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Consensus amyQ promoter.
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                   63
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                   BP;
                   Sequence 185
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region and TATAAT for the -10 region. The method further comprises isolating the polypeptide from the cultivation medium. The method is useful for producing a polypeptide in a Bacillus strain. The present sequence is Bacillus amyloliquefaciens alpha-amylase (amy) consensus mutated promoter, used in the exemplification of the invention
                                                                                                                                                                                                                                                     crercarcadacadecrarrirrarecrereccadecrerececrereranananada
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                                                                                                                         Score 185; DB 4; Length 185; Pred. No. 1.6e-41;
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                                                                                           Sequence 185 BP; 63 A; 25 C; 42 G; 55 T; 0 U; 0 Other;
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                                                                                                                                                         0; Mismatches
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Matches 185;
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the
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to describe the
                                                             Length
                                                                                     Indels
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                                    42 G; 56 T; 0 U; 0 Other;
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                                                             DB 2;
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                                                           Score 183.4; DB 2
Pred. No. 4.4e-41;
                                                                                    Mismatches
alpha-amylase amyQ promoter which is used
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Best Local Similarity 99.5%;
Matches 184; Conservative 0
                                      62 A; 25 C;
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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                      Conservative
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                                                                         Similarity
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                                      Sequence 185 BP;
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                                                                                      Matches 184;
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              invention
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Best Local (
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This invention describes a novel method for the production of a polypeptide in Bacillus using specific tandem or consensus promoters. The method is used to produce homologous or particularly heterologous proteins, particularly enzymes (specifically serine protease, maltogenic alpha-amylase and pullulanase), but also hormones, antibodies, reporters etc. The specified promoters provide increased expression of the sequence
                                                                                                                                                                                                                                                                                                                                                        ATAAAGGGGGGTTGACATTATTTACTGATATGTATAATAATTTGTATAAGAAAATGG 180
promoter comprises amyL promoter, amyQ promoter, aprH promoter, cryIIIA promoter or subtilisin Carlsberg gene promoter. The consensus promoters of the amyL promoter, amyQ promoter, pryIIIA promoter or subtilisin Carlsberg gene promoter have the sequence TYCACA for the 35 region and TATAAT for the -10 region. The method further comprises isolating the polypeptide from the cultivation medium. The method is useful for producing a polypeptide in a Bacillus strain. The method is sequence is Bacillus amyloliquefaciens alpha-amylase (amyQ) consensus mutated promoter, used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                               CTGTCATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAAAGGA
                                                                                                                                                                                                                                                                                                                             Tandem promoter; consensus promoter; enzyme production; hormone; antibody; reporter; marker gene; cell regulation; alpha-amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Production of polypeptide in Bacillus using specific promoters, particularly for producing enzymes.
                                                                                                                                                                            99.1%; Score 183.4; DB 4; Length 185; 99.5%; Pred. No. 4.4e-41;
                                                                                                                                                                                                          Indels
                                                                                                                                                Sequence 185 BP; 62 A; 25 C; 42 G; 56 T; 0 U; 0 Other;
                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amyQ promoter consensus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 21; 90pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                             Matches 184; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-561370/47
                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-SEP-1999.
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                                                                                                                                                                                Query Match
Best Local S
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                                                                                                                                        180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for producing a polypeptide, comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters. The Bacillus is cultivated in a medium conducive for the production of the polypeptide. Each promoter sequence of the tandem promoter is operably linked to a nucleic acid sequence encoding the polypeptide. The tandem
                                                                                                   GGCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAGAAGAAGAAGAAGAAGAAATAAAAATACCTTGT
                                                                                ATAAAGGGGGGTTGACATTATTTTACTGATATGTATAATATATTTTGTATAAGAAAATGG
                                                                                                                                                                                                                                                                                                                                                                                          Bacillus amyloliquefaciens alpha-amylase (amyQ) consensus promoter #2.
                       GGCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAGAAGAAGAAGACATAAAAATACCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus cell, tandem promoter; consensus promoter; mutant; polypeptide production; amyL promoter; amyQ promoter; aprH promoter; cryIIIA promoter; subtilisin Carlsberg gene promoter; alpha-amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing a polypeptide in a Bacillus strain comprises cultivating Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters.
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replace(135, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    replace (156, A)
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                                                                                                                                                                                                                                                                                                       AAD09924 standard; DNA; 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                 AGCTC 185
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/note= "Base T is found at this location in the sequence
shown in the sequence listing of the specification
(AAD09222)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus cell; tandem promoter; consensus promoter; polypeptide production; amyL promoter; amyQ promoter; aprH promoter; cryIIIA promoter; subtilisin Carlsberg gene promoter; alpha-amylase; ds.
which encodes the polypeptide of the invention. After incorporation of the nucleic acid construct of the invention, any marker gene may be deleted, resulting in a cell that is preferred for environmental and regulatory regions. This sequence represents the consensus sequence of Bacillus sp. alpha-amylase amyQ promoter which is used to describe the
                                                                                                                                                                                                GGCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAGAAGAAGAGACCATAAAAATACCTTGT
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                                                                                                                      Length 185;
                                                                                                                                               Indels
                                                                                           Sequence 185 BP; 63 A; 24 C; 42 G; 56 T; 0 U; 0 Other;
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                                                                                                                 Score 180.2; DB 2
Pred. No. 3.3e-40;
); Mismatches 3
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                                                                                                                      .48;
                                                                                                                                98.4%;
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                                                                                                               Query Match
Best Local Similarity 98.4°
Matches 182; Conservative
                                                                 method of the invention
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                                                                                                                                                                                                                                                                                                                                    185
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misc_feature
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The present invention relates to a method for producing a polypeptide, comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters. The Bacillus is cultivated in a medium conducive for the production of the polypeptide. Bach promoter sequence of the tandem promoter is operably linked to a nucleic acid sequence encoding the polypeptide. The tandem promoter comprises amyL promoter, amyQ promoter, aptH promoter, cryllia promoter, anyQ promoter, aptH promoter, cryllia promoter or subtilisin Carlaberg gene promoter. The consensus promoters of the amyL promoter, anyQ promoter, have the sequence Troatca for the -35 region and TAFART for the -10 region. The method further comprises isolating the polypeptide from the cultivation medium. The method is useful for producing a polypeptide in a Bacillus strain. The present sequence is an alternative of Bacillus amyloliquefaciens alpha-amylase (amyQ) promoter, used in the exemplification of the invention. Note: This sequence is stated as being the same as that shown as SEQ ID NO 25 (AAD09922) in column 43.44 of the specification. However the sequences
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                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                               Sequence 185 BP; 63 A; 24 C; 42 G; 56 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                              Score 180.2; DB 4
Pred. No. 3.3e-40;
0; Mismatches 3

    B. thuringiensis wild-type amyQ promoter DNA.

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                                                                                                                                                                                                                                                                                                              differ by at position 116
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Best Local Similarity 98.4
Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-561370/47.
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                                                                                                                                                        Similarity
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                                                                                                                                          Query Match
Best Local &
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                                                      polypeptide in Bacillus using specific tandem or consensus promoters. The method is used to produce homologous or particularly heterologous proteins, particularly energians proteins, particularly enzymes (specifically serine protease, maltogenic alpha-amylase and pullulanase), but also hormones, antibodies, reporters etc. The specified promoters provide increased expression of the sequence which encodes the polypeptide of the invention. After incorporation of the nucleic acid construct of the invention, any marker gene may be deleted, resulting in a cell that is preferred for environmental and regulatory regions. This sequence represents a Bacillus thuringianals alpha-amylase amyQ promoter which is used to describe the method of the
                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAAAGGGGGTTGTTATTTTATTTTACTGATATGTAAAATATAATTTGTATAAAGAAAATGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAAAGGGGGGTTGACATTATTTTACTGATATGTATAATATAATTTGTATAAGAAAATGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated polypeptide having pectin acetylesterase activity useful for degrading pectic substances and in degradation or modification of acetylated pectins and plant cell walls.
                                                                                                                                                                                                                                                                                                                                                                              CTGTCATCAGACAGGGTATTTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAAAGGA
                                                                                                                                                                                                                                                                                                                    Gaps
                                         This invention describes a novel method for the production of a
                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                           DB 2; Length 185;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                               Seguence 185 BP; 62 A; 24 C; 42 G; 57 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pectin acetylesterase; degrade; plant cell wall;
                                                                                                                                                                                                                                                                          .2e-40;
                                                                                                                                                                                                                                                           Score 178.6;
Pred. No. 9.26
0; Mismatches
             Disclosure; Page 90; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVO ) NOVO NORDISK BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 9; Fig 9; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                         96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-00384305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF62645 standard; DNA; 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wild type amyQ promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brown KM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-190946/19.
                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCTC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCTC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6184028-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-2001
                                                                                                                                                                                                                                                                                     Matches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thomas MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                    н
                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF62645;
                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to Bacillus subtilis pectin acetylesterase protein. The invention is useful for degrading a pectic substance. It is also useful for degrading soluble and insoluble pectins with varying degrees of esterification, clarification etc. The protein may be used alone or in combination with other enzymes for the degradation or modification of acetylated pectins, degradation or modification of plant
                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus cell; tandem promoter; consensus promoter; aprH promoter; polypeptide production; amyL promoter; amyQ promoter; aprH promoter; cryIIIA promoter; subtilisin Carlsberg gene promoter; alpha-amylase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for producing a polypeptide, comprises cultivating a Bacillus cell, which contains a mucleic acid construct comprising a tandem promoter and consensus promoters. The Bacillus is cultivated in a medium conducive for the production of the polypeptide. Each promoter sequence of the tandem promoter is operably linked to a nucleic acid sequence encoding the polypeptide. The tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAAAGGGGGGTTGACATTATTTACTGATATGTATAATATTTGTATAAGAAAATGG
                                                                                                                                                                                                                                                                                                                     GCCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAAGAAGAAGAAGACCATAAAAATACCTTGT
                                                                                                                                                                                                                                                                                            GGCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAAGAAGAGACCATAAAAATACCTTGT
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing a polypeptide in a Bacillus strain comprises cultivating Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters.
                                                                                                                                                                                                                                                       ·
0
                                                                                                                                                                                                            4; Length 185;
                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus amyloliquefaciens alpha-amylase (amyQ) promoter.
                                                                                                                                                                      Sequence 185 BP; 62 A; 24 C; 42 G; 57 T; 0 U; 0 Other;
                                                                                                                                                                                                            Score 178.6; DB 4
Pred. No. 9.2e-40;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 18; Col 43-44; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD09922 standard; DNA; 185 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thomas MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVO ) NOVOZYMES BIOTECH INC.
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                                                                                                                                                                                                            96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                       181; Conservative
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                   134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening protease/protease inhibitor gene library for gene encoding the same, by constructing host cell having the gene, cultivating cell, dissociating complex formed between them, selecting protein and isolating
                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protease; screening; barley; chymotrypsin inhibitor; CI-2A; laundry; detergent industry; dishwash; fabric softener; subtilisin 309; savinase; chimeric; ds.
promoter comprises amyL promoter, amyQ promoter, aprH promoter, crylIIA promoter or subtilisin Carlsberg gene promoter. The consensus promoters of the amyL promoter, amyQ promoter, aprH promoter, crylIIA promoter or subtilisin Carlsberg gene promoter have the sequence TTGACA for the -35 region and TATAAT for the -10 region. The method further comprises isolating the polypeptide from the cultivation medium. The method is sequence is Bacillus amyloliquefaciens alpha-amylase (amyQ) promoter, used in the exemplification of the invention. Note: This sequence is stated as being the same as that shown as SEQ ID NO 25 (AAD09931) in figure 21 of the specification. However the sequences differ by at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-terminal Subtilisin 309-CI-2A fusion protein encoding construct A DNA
                                                                                                                                                                                                                GGCCTTAAGGGCCTGCAATCGATTGTTTGAGAAAAAAAAGAAGAACATAAAAATACCTTGT
                                                                                                                                                                                                                                        cretcarcagacaggerarrirrargecrerccagacreccecrereraaaaarraga
                                                                                                                                                                                               GGCCTTAAAGGGCCTGCAATCGATTGTTTGAGAAAAAAGAAGAAGAACATAAAAATACCTTGT
                                                                                                                                                                            Gaps
                                                                                                                                                                           .
                                                                                                                                                        DB 4; Length 185;
                                                                                                                                                                            Indels
                                                                                                                                  Sequence 185 BP; 62 A; 24 C; 42 G; 57 T; 0 U; 0 Other;
                                                                                                                                                                            4,
                                                                                                                                                     Score 178.6; DB 4
Pred. No. 9.2e-40;
0; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                            ВЪ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Norregaard-Madsen
                                                                                                                                                                                                                                                                                                                                                                                            AAD34433 standard; DNA; 2166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-2001; 2001WO-DK000503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-AUG-2000; 2000DK-00001273.
05-SEP-2000; 2000US-0230017P.
                                                                                                                                                      Ouery Match
Best Local Similarity 97.8%;
Matches 181; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVO ) NOVOZYMES AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-329776/36.
                                                                                                                                                                                                                                                                                                                       AGCIC 185
                                                                                                                                                                                                                                                                                                                                           AGCTC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordeum sp.
Bacillus lentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200218588-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pedersen PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                    29-AUG-2003
16-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                AAD34433;
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                                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                         181
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                                                                                                                                                                                                                                                                                                                                                                                    AAD34433
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The invention relates to a method for screening a protease/protease conhibitor gene library for a gene encoding a protease of interest. The method comprises introducing a first gene of the protease gene library and a second gene encoding a protease inhibitor into a host cell; and a second gene encoding a protease inhibitor into a host cell; cultivating the host cell, wherein the cell expresses the first and the cecond genes to produce a complex of a protease and the inhibitor; dissociating the inhibitor from the complex and selecting the protease of interest and isolating the encoding gene. A complex may be used for a number of industrial applications, in particular within the detergent of industry, thus, relates to a cleaning or detergent composition, or perferably a laundry or dishwash composition including a laundry or dishwash composition including a laundry additive composition, or be formulated as a detergent composition for use in general household hard surface cleaning operations or be formulated for hand or machine dish washing operations. The present sequence is a construct encoding a fusion protein containing C-terminal region of subtilisin 309 (savinase) and barley chymotrypsin inhibitor CI-containing C-terminal collicial)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 GGGTATITITIANGCTGTCCAGACTGTCCGCTGTGTAAAAAAAGGAAATAAAGGGGGGGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protease; allergenicity; detergent; subtilase; Sl1; Sl2; additive; protease inhibitor; barley; chymotrypsin; Cl-2A; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 159.6; DB 6; Length 2166; Pred. No. 2.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 GTTATTTTTACTGATATGTAAATATATATTTGTATAAGAAATG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACATTATTTTACTGATATGTATATATATTTGTATAAGAAATG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2166 BP; 610 A; 442 C; 582 G; 532 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              construct A comprising Savinase-CI-2A fusion sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
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Example 1; Page 47-48; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protease inhibitor; barley; chymot;
subtilisin; savinase; apr gene; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-2001; 2001WO-DK000479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000DK-00001233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.6%;
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVO ) NOVOZYMES AS
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24-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-2002
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21-AUG-2000; 2000DK-00001233
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                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL40499
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                                                                                                                                                                                                                                                                                                                        The invention provides a method for producing a protease-inhibitor complex with reduced allergenicity for use in detergents. The method involves (a) constructing a fusion polynucleotide sequence in frame, the sequence comprising a first gene encoding a protease (preferably a bublishes S11 or S12) and a second gene encoding a protease inhibitor; (b) introducing the sequence into a host cell, and (c) cultivating the host cell expresses the sequence an produces a non-covalently linked complex of the protease and the inhibitor. The protease—inhibitor complex produced by the method may be used as an nucleotide sequence of a DNA construct comprising the savinase-CI-2A
                                                                                                                                                                                                                                                                               73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease; screening; barley; chymotrypsin inhibitor; CI-2A; laundry; detergent industry; dishwash; fabric softener; subtilisin 309; savinase; chimeric; ds.
                                                                                                                                                                                                                                                                                                    rgcaarcgarrgraaaagaagaagaccaraaaaaraccrrgrcrrgrcrrgrcagaca
                                                                                                                                                                                                                                                                               Subtilisin 309-CI-2A transcriptional product encoding construct B DNA
                                       Producing protease-inhibitor compositions with reduced allergenicity, stability and activity for use in detergent compositions.
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                   Score 159.6; DB 6; Length 2166; Pred. No. 2.8e-34; 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                  134 GACATTATTTTACTGATATGTATATATATTTGTATAAGAAAATG 179
                                                                                                                                                                                                                                                                                                                                                                                   GTTATTATTATTACTGATATGTAAATATATTTGTATAGAAAATG 337
                                                                                                                                                                                                                  Sequence 2166 BP; 610 A; 442 C; 582 G; 532 T; 0 U; 0 Other;
                                                                       Example 1; Page 45-46; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pedersen PE, Norregaard-Madsen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUL-2001; 2001WO-DK000503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-2000; 2000DK-00001273.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD34434 standard; DNA; 2267
                                                                                                                                                                                                                                       86.3%;
97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                              Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-329776/36.
                     WPI; 2002-242031/29.
                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hordeum sp.
Racillus lentus.
                                                                                                                                                                                                 fusion sequence
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The invention relates to a method for screening a protease/protease method comprises introducing a first gene of the protease gene library method comprises introducing a first gene of the protease gene library and a second gene encoding a protease inhibitor into a host cell, wherein the cell expresses the first and the second gene encoding a protease inhibitor. The cell, wherein the cell expresses the first and the second genes to protease and the inhibitor, dissociating the inhibitor from the complex and selecting the protease of interest and isolating the encoding gene, A complex may be used for a number of industrial applications, in particular within the detergent ondustry, thus, relates to a cleaning or detergent composition, preferably a laundry or dishwash composition comprising the complex, where hand or machine laundry detergent composition including a laundry detergent composition suitable for pre-treatment of stained fabrics and a rise added composition, or be formulated as a detergent composition for use in general household hard surface cleaning operations. The present sequence is a construct encoding a transcriptional fusion product containing C-terminal region of subtilisin 309 (savinase) and barley chamber of the further of the complex of the composition inhibitor CI-2A protein used in the invention. (Updated on C 29-AUG-2003 to standardise OS field)
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Screening protease/protease inhibitor gene library for gene encoding the same, by constructing host cell having the gene, cultivating cell, dissociating complex formed between them, selecting protein and isolating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2267 BP; 640 A; 462 C; 601 G; 564 T; 0 U; 0 Other;
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0; Mismatches
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                                                                                                                                                                                         Example 1; Page 48; 54pp; English
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Hordeum sp.
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PR 24-AUG-2000; 2000US-022750IP.

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Producing procease-inhibitor compositions with reduced allergenicity, at activity for use in detergent compositions.

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Producing procease-inhibitor compositions with reduced allergenicity, producing procease-inhibitor complex with reduced allergenicity for use in detergent compositions.

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Example 1; Page 46; 52pp; English.

XX
CC complex with reduced allergenicity for use in detergenicity, procease inhibitor complex with reduced allergenicity for use in detergence in frame, the complex with reduced allergenicity for use in detergence in frame, the complex with reduced allergenicity for use in detergence in frame, the complex with reduced allergenicity for use in detergence in frame, the sequence comprising a first gene encoding a procease inhibitor; (C) introducing the sequence into a host cell; and (C) cultivating the host cell (the host cell expresses the sequence an produces a noncovalently linked complex protease and the inhibitor; The protease and the inhibitor; The protease and the inhibitor. The protease and the inhibitor of a DNA construct comprising the savinase-CI-2A (sequence 2267 BP; 640 A; 462 C; 601 G; 564 T; 0 U; 0 Other;
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Search completed: March 19, 2004, 01:38:17 Job time : 218 secs

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March 19, 2004, 00:23:20; Search time 1078.5 Seconds (without alignments) 7434.827 Million cell updates/sec
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185
1 ggccttaagggcctgcaatc......tgtataagaaaatggagctc 185
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

G G	ARI60502 Sequence AX088920 Sequence BD136798 Process f AX088921 Sequence BD136799 Process f AX160501 Sequence AX088919 Sequence AX088919 Sequence AX088919 Sequence AX088919 Sequence AX088919 Sequence AX088919 Sequence AX088919 Sequence AX088919 Sequence AX088919 Sequence AX088919 Sequence AX088919 Sequence AX088919 Sequence AX088919 Sequence AX088919 Sequence AX088919 Sequence AX08891 Sequence	A00156 Nucleotide A00158 Nucleotide A00158 Nucleotide A00158 Nucleotide A00158 Nucleotide A00158 Sucleotide A00604 B.amyloliqu A00605 B.amyloliqu A00605 B.amyloliqu A00152 Bedilus am AR008285 Sequence AR13795 Sequence AR13795 Sequence AR13795 Sequence AR234265 Sequence AR234261 Sequence AR242861 Sequence AR242861 Sequence AR242861 Sequence AR242861 Sequence AX33926 Sequence AX33926 Sequence AX30926 Sequence AX30926 Sequence AX30926 Sequence AX30926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence AX31926 Sequence	ar PAT 17-0CT-2001
			DNA linear in a Bacillus
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Bacillus
JP 200204379-A/26
JP 200204302
26-FEB-1999 UP 2000533574
26-FEB-1999 US 09/031442
MILLIAM WIDNER, ALLOMA, MICHABL D THOMAS
CI2NIS/09, CI2NI/21, CI2N9/54//C07K14/325, (CI2NI/21, CI2R1:07),
CI2NIS/00
Process for producing polypeptide in bacillus cells FH Key
Location/Qualifiers
N Process for producing polypeptide in bacillus cells. BD136798 BD136798 BD136798 BD136798 GL GI:23231743

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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
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Polypeptides having pectin acetylesterase activity and acids encoding same
Patent: WO 0114534-A 21 01-MAR-2001;
Novozymes Biotech, Inc. (US)
Location/Qualifiers
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Best Local Si
Matches 185;
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Length 185;
100.0%; Score 185; DB 6; Length 1.
llarity 100.0%; Pred. No. 7.2e-35;
Conservative 0; Mismatches 0; Indels
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Unknown.
Unclassified.
2 1 (bases 1 to 185)
S Widner, M. Sloma, A. and Thomas, M.D.
Methods for producing a polypeptide in
Methods for producing a polypeptide in
Location/Qualifiers
Location/Qualifiers
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Sequence 27 from patent US 6255076.
AR160503
AR160503.1 GI:16224480
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/mol_type="unassigned DNA"
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DNA

BD136798

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PAT 17-0CT-2001
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12-FEB-2002

26-FEB-1999 JP 2000533574

26-FEB-1998 US 09/031442

MILLIAM WIDNER,ALAN SLOMA,MICHAEL D THOMAS

C12N15/09,C12N1/21,C12N9/54//C07K14/325,(C12N1/21,C12R1:07),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIGICALCAGACAGGGTATITITATGCTGTCCAGACTGTCCGCTGTGTAAAAATAGGA
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Unclassified.
Unclassified.
1 (bases 1 to 185)
Widner, W., Sloma, A. and Thomas, M.D.
Wethods for producing a polypeptide in a Bacillus cell
Patent: US 6255076-A 25 03-JUL-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        Length 185;
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            1 (bases 1 to 185)
Widner,W., Sloma,A. and Thomas,M.D.
Process for producing polypeptide in bacillus cells
Patent: JP 2002504379-A 27 12-FEB-2002;
NOVO NORDISK BIOTECH INC
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Pred. No. 2.6e-33;
0; Mismatches 4;
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6
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Pred. No. 1.8e-34;
0; Mismatches 1
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/mol_type="unassigned DNA"

    .185
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

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Best Local Similarity 97.8
Matches 181; Conservative
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AR160501
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              Indels
 Pred, No. 1.8e-34;
D; Mismatches 1;
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    .185
    /organism="Bacillus subtilis"
/mol_type="unassigned DNA"
/db xref="taxon:1423"

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Sequence 22 from Patent WO0114534.
AX088921
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99.5%;
Best Local Similarity 99.5
Matches 184; Conservative
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Bacillus subtilis
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BD136799
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PAT 13-MAY-1997
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(hases 1 to 162)
Sloma,A.P., Outtrup,H., Dambmann,C. and Asslyng,D.A.
Nucleic acid constructs for the production of a Bacillus alkaline
Bacillus
JD 2002504379-A/25
12-FEB-2002
26-FEB-1999 JP 2000533574
26-FEB-1999 US 09/031442
MILLIAM WIDNER,ALAN SLOMA,MICHAEL D THOMAS
G12N15/09,C12N1/21,C12N9/54//C07K14/325,(C12N1/21,C12R1:07),
C12N15/09,C13N1/21,C12N9/54//C07K14/325,(C12N1/21,C12R1:07),
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/organism='Bacillus'
Location/Qualifiers
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Pred. No. 2.6e-
0; Mismatches
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Location/Qualifiers
1. 162
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 bp
Sequence 24 from patent US 5621089.
140596.1 GI:2082888
                                                                                                                                                                                      1. .185
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Best Local Simi
Matches 181; (
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Polypeptides having pectin acetylesterase activity and nucleic acids encoding same
Patent: WO 011453-A 20 01-MAR-2001;
Novozymes Biotech, Inc. (US)
Location/Qualifiers
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                     CTGTCATCAGACAGGGTATTTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAAAGGA
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Bacteria, Firmicutes; Bacillales; Bacillaceae, Bacillus.
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Widner, W., Sloma, A. and Thomas, M.D.
Process for producing polypeptide in bacillus cells
Parent: JP 2002504379-A 25 12-FEB-2002;
NOVO NORDISK BIOTECH INC
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96.5%; Score 178.6; DB 6; Length
Best Local Similarity 97.8%; Pred. No. 2.6e-33;
Matches 181; Conservative 0; Mismatches 4; Indels
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/mol_type="unassigned DNA"
/db_xref="taxon:1423"
                                                                                                                                                                                                                                   AX088919 185 bp
Sequence 20 from Patent WO0114534.
AX088919
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PAT 18-MAR-2003
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I (bases 1 to 162)

Sloma, A.P., Outtrup, H., Dambmann, C. and Aaslyng, D.Anita.
Sloma, A.P., Outtrup, H., Dambmann, C. and Saslyng, D.Anita.
Sloma, A.P., Outtrup, H., Dambmann, C. and Basillus alkaline protesses and vectors comprising same
Patent: US 5650326-A 24 22-UUL-1997;
Location/Qualifiers
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                                                                                                                TTATTTTACTGATATGTATATATATTTGTATAAGAAAATG
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llarity 97.5%; Pred. No. 1.1e-27;
Conservative 0; Mismatches 4;
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 24 from patent US 5650326.
156837
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                                                                                                                                                                                                                                                                                                                                                                 Unknown.
Unclassified.
Unclassified.
Unclassified.
Sloma, A.P., Outtrup, H., Dambmann, C. and Aaslyng, D.A.
Sloma, A.P., Outtrup, H., Dambmann, C. and Aaslyng, D.A.
Method for the production of heterologous polypeptides using a promoter element and signal peptide of a bacillus gene encoding an alkaline protease.
Patent: US 5522841-A 24 22-APR-1997;
Location/Qualifiers
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1 (bases 1 to 162)
Sloma,A.P., Outtrup,H., Dambmann,C. and Aaslyng,D.A.
Recombinant methods for the production of a bacillus alkaline
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         138 ITATITIACIGATAIGTATAATATATTIGTATAAGAAAAIG 179
                                          TTATTTTACTGATATGTAAAATATAATTTGTATAAGAAAATG 162
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Pred. No. 1.1e-27;
0; Mismatches 4;
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Best Local Similarity 97.5%; Pred. No. 1.1e-27;
Matches 158; Conservative 0; Mismatches 4
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Patent: US 5622850-A 24 22-APR-1997;
Location/Qualifiers
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requence 24 from patent US 5622841.
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|organism="unknown"
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ilarity 97.5%;
Conservative (
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amylase; amylase-alpha; signal peptide.

Bacillus amyloliquefaciens

Bacillus amyloliquefaciens

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

1 (bases 1 to 53?)

Palval., Pettersenon,R.F. Kalkkinen,N., Lehtovaara,P., Sarvas,M.,

Boderlund,H., Takkinen,R. and Kaariainen,L.

Nucleotide sequence of the promoter and NH2-terminal signal peptide
region of the alpha-amylase gene from Bacillus amyloliquefaciens

Gene 15 (1), 43-51 (1981)
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250. .342
/note="signal peptide"
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1. .249
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                                                                                                                                    84.1%; Score 155.6; DB 6; Length 249; llarity 97.5%; Pred. No. 9.7e-28; Conservative 0; Mismatches 4; Indels 0.
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